



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 160235

TO: Sumesh Kaushal
Location: REM-2B85/2C70
Art Unit: 1636
Monday, April 11, 2005

Case Serial Number: 09/925674

From: Deirdre Arnold
Location: Biotech-Chem Library
REM 1A64
Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

RUSH

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards,
Deirdre Arnold



This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 14:45:43 ; Search time 3068.26 Seconds

(without alignments)
9206.966 Million cell updates/sec

Title: US-09-925-674B-6

Perfect score: 583
Sequence: 1 atggcgacccagcagctgcgc.....cttttctgtagcaagtga 583

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Genbank1:*
1: gb ba:*
2: gb hta:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 583 | 100.0 | 583 | 6 | AX022529 Sequence |
| 2 | 583 | 100.0 | 583 | 6 | AX030817 Sequence |
| 3 | 577.2 | 99.0 | 582 | 6 | AX481423 Sequence |
| 4 | 577.2 | 99.0 | 582 | 9 | HSUS5747 |
| 5 | 575 | 98.6 | 3542 | 9 | D87461 Homo sapien |
| 6 | 572.4 | 98.2 | 582 | 6 | CQ730429 Sequence |
| 7 | 567.8 | 97.4 | 579 | 6 | AR020780 |
| 8 | 527.6 | 90.5 | 582 | 10 | AF086291 Rattus no |
| 9 | 527.6 | 90.5 | 1110 | 10 | AY185100 Rattus no |
| 10 | 527.6 | 90.5 | 3487 | 10 | AY185098 Rattus no |
| 11 | 527.6 | 90.5 | 3545 | 10 | BC074021 Rattus no |
| 12 | 523 | 89.7 | 579 | 6 | AR020779 Sequence |
| 13 | 522.8 | 89.7 | 582 | 10 | MMU59746 Mus muscu |
| 14 | 522.8 | 89.7 | 3476 | 10 | AF030769 Mus muscu |
| 15 | 511.8 | 87.8 | 3442 | 10 | AK172925 Mus muscu |
| 16 | 510 | 87.5 | 3473 | 10 | AY170344 Mus muscu |
| 17 | 501 | 85.9 | 581 | 6 | AX025531 Sequence |
| 18 | 501 | 85.9 | 581 | 6 | AX030819 Sequence |
| 19 | 441.2 | 75.7 | 220818 | 2 | AC128940 Rattus no |

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| 20 | 441.2 | 75.7 | 223933 | 2 | AC097389 Rattus no |
| 21 | 424 | 72.7 | 1098 | 6 | AR432565 Sequence |
| 22 | 424 | 72.7 | 1098 | 6 | BD078624 Human pro |
| 23 | 423.6 | 72.7 | 1864 | 6 | BD191165 186 human |
| 24 | 423.6 | 72.7 | 1864 | 6 | AX924675 Sequence |
| 25 | 423.4 | 72.6 | 196292 | 9 | CNS0000B |
| 26 | 383.8 | 65.8 | 148278 | 2 | AC079885 Human chr |
| 27 | 383.8 | 65.8 | 180665 | 2 | AC079885 Rattus no |
| 28 | 383.8 | 65.8 | 210784 | 2 | AC134055 Rattus no |
| 29 | 381.8 | 65.5 | 210784 | 2 | AC119293 Rattus no |
| 30 | 381.8 | 65.5 | 263901 | 2 | AC115371 Rattus no |
| 31 | 375.4 | 64.4 | 3815 | 10 | BC040369 Mus muscu |
| 32 | 375.4 | 64.4 | 237561 | 10 | AC116591 Mus muscu |
| 33 | 308 | 52.8 | 505 | 10 | AY185099 Rattus no |
| 34 | 255.4 | 43.8 | 6049 | 6 | AX345130 Sequence |
| 35 | 238.2 | 40.9 | 749 | 5 | XR1 Rattus no |
| 36 | 238.2 | 40.9 | 1894 | 5 | BC084445 Xenopus t |
| 37 | 236.6 | 40.6 | 1053 | 5 | BC073259 Xenopus t |
| 38 | 219.8 | 37.7 | 6049 | 6 | AX345131 Sequence |
| 39 | 150 | 25.7 | 150 | 6 | CQ055111 Sequence |
| 40 | 150 | 25.7 | 150 | 6 | CQ074369 Sequence |
| 41 | 150 | 25.7 | 150 | 6 | CQ105265 Sequence |
| 42 | 150 | 25.7 | 150 | 6 | CQ143959 Sequence |
| 43 | 150 | 25.7 | 150 | 6 | CQ179440 Sequence |
| 44 | 150 | 25.7 | 150 | 6 | CQ203800 Sequence |
| 45 | 150 | 25.7 | 150 | 6 | CQ227167 Sequence |

ALIGNMENTS

RESULT 1
LOCUS AX022529 583 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 6 from Patent EP0932674.
ACCESSION AX022529
VERSION AX022529.1 GI:10046125

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1
Adams, J. M., Holmgren, S. P., Cory, S. and Gibson, L. M.
A novel mammalian gene, bcl-2, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: EP 0932674-A 6 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
Location/Qualifiers
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CDS

ORIGIN

Query Match 100.0%; Score 583; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.5e-121;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGCGACCCAGCCTCGGCGCCAGACACGCGGCTCTGGTGACAGCTTGAGGTTAT 60
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Db 61 AAGCTGAGGACAGAGGGTATATGCTGTGAGCTTGCGCCCGGGAGGGCCAGCAGCTGAC 120
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Db 541 GGGGCCCTGTGATCTGTAGGGGCTTTTGTGCTAGCAAGTGA 583

RESULT 2
AX030817 583 bp DNA linear PAT 20-SEP-2000
LOCUS Sequence 6 from Patent W09735971.
DEFINITION AX030817
ACCESSION AX030817.1 GI:10278311
VERSION
KEYWORDS
SOURCE unidentifed
ORGANISM unidentifed
REFERENCE unclassified.
AUTHORS 1
TITLES
JOURNAL

FEATURES
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ORIGIN

Query Match 100.0%; Score 583; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.5e-121;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGGGCAACCCAGCCTCGGCCCCAGACACACGGGCTGTGAGCAGACTTTGTAGTTAT 60

Db 1 ATGGGCAACCCAGCCTCGGCCCCAGACACACGGGCTGTGAGCAGACTTTGTAGTTAT 60
QY 61 AACCTGAGCACAAGGCTTATATCTGTGAGCTGCGCCCGGGAGGGCCAGCAGCTGAC 120
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RESULT 3
AX481423 582 bp DNA linear PAT 16-AUG-2002
LOCUS Sequence 37 from Patent W02055693.
DEFINITION AX481423
ACCESSION AX481423.1 GI:22316337
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Kreutzer, R., Lommer, S., Roel, S. and Hadwiger, P.
AUTHORS Method for inhibiting the expression of a target gene
TITLES Patent: WO 02055693-A 37 18-JUL-2002;
JOURNAL Ribopharmma AG (DE)
FEATURES
source
1. 582
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Query Match 99.0%; Score 577.2; DB 6; Length 582;
Best Local Similarity 99.5%; Pred. No. 7.2e-120;
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QY 61 AAGCTGAGCAGAAAGGTTATATGCTGTGAGCTTGCGCCCGGGAGGGCCAGCAGCTGAC 120

Db 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGAGCTGAGCCCGGGAGAGGGCCAGACAGTGTAC 120
Qy 121 CCGCTGACCAAGCATGCGGCGAGCTGTGAGATGATGTTCCAGACCCGCTTCCGGCGAC 180
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Qy 361 CAAGTGAAGAGTGTGAGTGTGCTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 420
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RESULT 4

HSUS9747

LOCUS HSUS9747 582 bp mRNA linear PRI 29-SEP-1996
DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION U59747
VERSION U59747.1 GI:1572492

KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 582)
Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,
Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M., and Cory, S.

1 (bases 1 to 582)
bcl-w, a novel member of the bcl-2 family, promotes cell survival
Oncogene 13 (4), 665-675 (1996)

REFERENCE
JOURNAL
MEDLINE
PUBMED
8761287

2 (bases 1 to 582)
Gibson, L., Holmgren, S.P., Huang, D.C.S., Bernard, O., Adams, J.M., and
Cory, S.

Direct Submission
Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
Eliza Hall Institute of Medical Research, PO Royal Melbourne
Hospital, Parkville, Victoria 3050, Australia

REFERENCE
AUTHORS
1. 582
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REFERENCE
AUTHORS
1 (bases 1 to 582)
Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,
Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M., and Cory, S.

1 (bases 1 to 582)
bcl-w, a novel member of the bcl-2 family, promotes cell survival
Oncogene 13 (4), 665-675 (1996)

REFERENCE
JOURNAL
MEDLINE
PUBMED
8761287

2 (bases 1 to 582)
Gibson, L., Holmgren, S.P., Huang, D.C.S., Bernard, O., Adams, J.M., and
Cory, S.

Direct Submission
Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
Eliza Hall Institute of Medical Research, PO Royal Melbourne
Hospital, Parkville, Victoria 3050, Australia

REFERENCE
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/organism="Homo sapiens"
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Query Match 99.5%; Score 577.2; DB 9; Length 582;
Best Local Similarity 99.5%; Pred. No. 7.2e-120;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGCCACCCCACTGGGCGCCGACACAGCGGCTCTGGTGCAGACTTGTAGCTTAT 60
Db 1 ATGGCCACCCCACTGGGCGCCGACACAGCGGCTCTGGTGCAGACTTGTAGCTTAT 60
Qy 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGTGTGAGCCCGGGAGAGGCCAGAGACTGAC 120
Db 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGTGTGAGCCCGGGAGAGGCCAGAGACTGAC 120
Qy 121 CCGCTGACCAAGCCATGCGGCGAGCTGTGAGATGATGATTCAGACCCGCTTCCGGCGAC 180
Db 121 CCGCTGACCAAGCCATGCGGCGAGCTGTGAGATGATGATTCAGACCCGCTTCCGGCGAC 180
Qy 181 TTCTCTATCTGGGCGCTCAGCTGATGTGACCCAGAGCTGAGCCAGCAACGCTTGACC 240
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Db 361 CAAGTGAAGAGTGTGAGTGTGCTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 420
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Db 481 CGTCTGCGGAGGAGGAACTGGGCACTGAGAGAGAGAGTGTGAGAGAGAGTGTGAGAG 540
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RESULT 5

DB87461

LOCUS DB87461 3542 bp mRNA linear PRI 10-JAN-2004
DEFINITION Homo sapiens mRNA for KIAA0271 gene, partial cds.
ACCESSION DB87461
VERSION DB87461.1 GI:1944417

KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 3542)
Nagase, T., Seki, N., Ishikawa, K., Ohira, M., Kawarabayashi, Y.,
Ohara, O., Tanaka, A., Kotani, H., Miyajima, N., and Nomura, N.

1 (bases 1 to 3542)
Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
analysis of cDNA clones from cell line KG-1 and brain

1 (bases 1 to 3542)
DNA Res. 3 (5), 321-329 (1996)

REFERENCE
JOURNAL
MEDLINE
PUBMED
97191544

2 (bases 1 to 3542)
Nagase, T., Seki, N., Ishikawa, K., Ohira, M., Kawarabayashi, Y.,
Ohara, O., Tanaka, A., Kotani, H., Miyajima, N., and Nomura, N.

1 (bases 1 to 3542)
Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
analysis of cDNA clones from cell line KG-1 and brain

| | |
|-----------|---|
| PUBMED | 9039502 |
| REFERENCE | 2 (bases 1 to 3542) |
| AUTHORS | Ohara, O., Nagase, T., Kikuno, R. and Nomura, N |
| TITLE | Direct Submission |
| JOURNAL | Submitted (27-AUG-1996) Osamu Ohara, Kazusa |

ORIGIN

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|---------------------------|--------|---------------------|-----------|--------------|
| Query Match | 98.6% | Score 575; | DB 9; | Length 3542; |
| Best Local Similarity | 99.1%; | Pred. No. 1.8e-119; | | |
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OY 541 GGGGCCCTGTAAGGCGCTTTTGTCTACCAAGTGAA 58
| | | | |
Dd 717 GGCGCCCTGTAAGGCGCTTTTGTCTACCAAGTGAA 755
| | | | |

[illegible]

REFERENCE
AUTHORS
TITLE

1 Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
Venter, C. J., Adams, M. C., Li, P. W., and Myers, E. W.
Kites, such as nucleic acid arrays, comprising a majority of
dinucleotides or trinucleotides.

ORIGIN

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Query Match      98.28; Score 572.4; DB 6; Length 582;
Best Local Similarity 99.04; Pred No. 8.8e-119;
Matches 576; Conservative 0; Mismatches 6; Indels 0; Gaps 0
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RESULT 7
AR020780
LOCUS AR020780 579 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5789201.
ACCESSION AR020780
VERSION AR020780.1 GI:3975395
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 579)
AUTHORS Guastella, J.
TITLE Genes coding for bcl-2 and bcl-2 homologue
JOURNAL Patent: US 5789201-A 2 04-AUG-1998;
FEATURES
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ORIGIN
Query Match 97.4%; Score 567.8; DB 6; Length 579;
Best Local Similarity 98.8%; Pred. No. 9.6e-118;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCAAGCTTGGGCCCCAGACACAGGGGCTCTGTGGGAGACTTTGTAGTTAT 60
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DB 121 CCACTGACCAAGCCATGCGGGAGCTGGAGATGATGATGAGACCCGCTTCGGCGCAC 180
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QY 301 CTCTTTGGGGCTGACATGTGTGCTGAGATGATCAAGAGATGAAACAAGTGGTGGGA 360
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QY 361 CAAGTGCAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 CAAGTGCAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 AGTGGGGGCTGGGGGAGTTCAAGCTTATACGGGGGAGGGGGGCTTGAAGAGAGGGGG 480
DB 421 AGTGGGGGCTGGGGGAGTTCAAGCTTATACGGGGGAGGGGGGCTTGAAGAGAGGGGG 480
QY 481 CGTCTGCGGAGAGGGGAACTGGGCAATCAAGTGAAGAGAGTGTGACGGGGGCGTGGCACTG 540
DB 481 CGTCTGCGGAGAGGGGAACTGGGCAATCAAGTGAAGAGAGTGTGACGGGGGCGTGGCACTG 540
QY 541 GGGGCGCTGTGATCTGTAGGGGGCTTTTGTCTGCAAG 579
DB 541 GGGGCGCTGTGATCTGTAGGGGGCTTTTGTCTGCAAG 579

RESULT 8
AF096291
LOCUS AF096291 582 bp mRNA linear ROD 28-FEB-2000
DEFINITION Rattus norvegicus Bcl-2 (bcl-2) mRNA, complete cds.
ACCESSION AF096291
VERSION AF096291.1 GI:3747129

KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE
AUTHORS Hammer, S., Skogjose, Y. and Lindholm, D.
TITLE Differential expression of bcl-2 and bcl-x messenger RNA in the developing and adult rat nervous system
JOURNAL Neuroscience 91 (2), 673-684 (1999)
MEDLINE 99292146
PUBMED 10366024
REFERENCE
AUTHORS Hammer, S., Skogjose, Y. and Lindholm, D.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala University, Box 587, BMC, Uppsala 751 23, Sweden
FEATURES
source 1.582
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
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ORIGIN
Query Match 90.5%; Score 527.6; DB 10; Length 582;
Best Local Similarity 94.2%; Pred. No. 1.1e-108;
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCAAGCTTGGGCCCCAGACACAGGGGCTCTGTGGGAGACTTTGTAGTTAT 60
DB 1 ATGGCGACCCCAAGCTTGGGCCCCAGACACAGGGGCTCTGTGGGAGACTTTGTAGTTAT 60
QY 61 AAGCTGAGGAGAGGTTATGTCTGTGAGCTGGGCCCCGGGGAGGGCCCCAGACAGTAC 120
DB 61 AAGCTGAGGAGAGGTTATGTCTGTGAGCTGGGCCCCGGGGAGGGCCCCAGACAGTAC 120
QY 121 CCGCTGACCAAGCCATGCGGGAGCTGGAGATGATGATGATGATGATGATGATGATGATGAT 180
DB 121 CCGCTGACCAAGCCATGCGGGAGCTGGAGATGATGATGATGATGATGATGATGATGATGAT 180
QY 181 TTCTCTGATCTGGGGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
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DB 241 CAGGCTCCGACGAAGCTTTTCAAGGGGGGCCCCAAGTGGGGGCGCTTGTAGCTTTCTT 300
QY 301 CTCTTTGGGGCTGACATGTGTGCTGAGATGATCAAGAGATGAAACAAGTGGTGGGA 360
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QY 421 AGTGGGGCTGGGCGGAGTTCAAGCTATATAGGGGACGGGGCCCTGGAGAGCGCGG 480
DB 421 AGTGGGGCTGGGCGGAGTTCAAGCTATATAGGGGAGCGGGCCCTGGAGAGCGCGG 480
QY 481 CGTCTGGCGGAGGAGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
DB 481 CGTCTGGCGGAGGAGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
QY 541 GGGGCCCTGTACTGTAGTGGGGCCCTTTTGTCTAGCAAGTGA 582
DB 541 GGGGCCCTGTACTGTAGTGGGGCCCTTTTGTCTAGCAAGTGA 582

RESULT 9 1110 bp mRNA linear ROD 24-JUN-2003
LOCUS AY185100
DEFINITION Rattus norvegicus BCL-WEL mRNA, complete cds.
ACCESSION AY185100
VERSION AY185100.1 GI:32185284
KEYWORDS

SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 1110)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Bcl-2-related protein family gene expression during
oligodendroglial differentiation
JOURNAL J. Neurochem. 85 (6), 1500-1512 (2003)
MEDLINE 22672518
PUBMED 12787069

REFERENCE 2 (bases 1 to 1110)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Neurology Research, The Children's Hospital
of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center
Blvd., Philadelphia, PA 19104, USA

FEATURES
source Location/Qualifiers
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K"
ORIGIN

Query Match 90.5%; Score 527.6; DB 10; Length 1110;
Best Local Similarity 94.2%; Pred. No. 1e-108;
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGGAGCCCAAGCTCGGCCCCAGACACAGGGCTCTGTGGCAGACTTTAGGTTAT 60
DB 509 ATGGGAGCCCAAGCTCGGCCCCAGACACAGGGCTCTGTGGCAGACTTTAGGTTAT 568
QY 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCCGGGGAGAGGCCCAAGAGCTGAC 120
DB 569 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCCGGGGAGAGGCCCAAGAGCTGAC 628
QY 121 CCGGTGACCAAGGATGCTGGCGGACGCTGAGATGAGTTGAGACCGCTTCGGCGGACAC 180
DB 629 CCGGTGACCAAGGATGCTGGCGGACGCTGAGATGAGTTGAGACCGCTTCGGCGGACAC 688
QY 181 TTCTGTATCTGGCGGCTCAGTGCATGTGTACCCCAAGGCTCAGCCCAAGCAAGCTTCAAC 240

DB 689 TTCTGTATCTGGCGGCTCAGTGCATGTGTACCCCAAGGCTCAGCCCAAGCAAGCTTCAAC 748
QY 241 CAGGTCTCCGAGCAACTTTTTCAGAGGGGCCCAACTGAGGGCCGCTTTAGACCTTTT 300
DB 749 CAGGTCTCCGAGCAACTTTTTCAGAGGGGCCCAACTGAGGGCCGCTTTAGACCTTTT 808
QY 301 CTCTTTGGGGCTGACCTGTGTGCTGAGAGTGTCAACAAGATGAGAACCACTGTGGGA 360
DB 809 GTCTTTGGGGCTGACCTGTGTGCTGAGAGTGTCAACAAGATGAGAACCACTGTGGGA 868
QY 361 CAAGTGCAGAGTGTGATGTGTGCTGACCTGAGAGACGCGGCTGTGATGATCCACAGC 420
DB 869 CAAGTGCAGAGTGTGATGTGTGCTGACCTGAGAGACGCGGCTGTGATGATCCACAGC 928
QY 421 AGTGGGGCTGGGGGAGTTTCAAGCTCTTTCAGGGGACGGGCCCTTGAAGAGGCGCG 480
DB 929 AGTGGGGCTGGGGGAGTTTCAAGCTCTTTCAGGGGACGGGCCCTTGAAGAGGCGCG 988
QY 481 CGTCTGGCGGAGGAGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
DB 989 CGTCTGGCGGAGGAGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 1048
QY 541 GGGGCCCTGTACTGTAGTGGGGCCCTTTTGTCTAGCAAGTGA 582
DB 1049 GGGGCCCTGTACTGTAGTGGGGCCCTTTTGTCTAGCAAGTGA 1090

RESULT 10 3487 bp mRNA linear ROD 24-JUN-2003
LOCUS AY185098
DEFINITION Rattus norvegicus BCL-W mRNA, complete cds.
ACCESSION AY185098
VERSION AY185098.1 GI:32185280
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 3487)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Bcl-2-related protein family gene expression during
oligodendroglial differentiation
JOURNAL J. Neurochem. 85 (6), 1500-1512 (2003)
MEDLINE 22672518
PUBMED 12787069

REFERENCE 2 (bases 1 to 3487)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Neurology Research, The Children's Hospital
of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center
Blvd., Philadelphia, PA 19104, USA

FEATURES
source Location/Qualifiers
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RLNEGMAVSRVTLTGAVALGALVTGAAFFAAK"
ORIGIN

Query Match 90.5%; Score 527.6; DB 10; Length 3487;
Best Local Similarity 94.2%; Pred. No. 9.1e-109;
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGGAGACCCAGGCTGGGCCCCAGACACAGGGGCTGTGNGGAGACTTTGATGTTAT 60
 DB 170 ATGGGAGACCCAGGCTGGGCCCCAGACACAGGGGCTGTGNGGAGACTTTGATGTTAT 229
 QY 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGAGGGCCAGAGCTGAC 120
 DB 230 AAGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGAGGGCCAGAGCTGAC 289
 QY 121 CCGCTGACCAAGCCATGCGGGGAGCTGGAGATGATGATGAGAGCCCGTTCCGGCGCAC 180
 DB 290 CCGCTGACCAAGCCATGCGGGGAGCTGGAGATGATGATGAGAGCCCGTTCCGGCGCAC 349
 QY 181 TTCTCTATCTGGGGGCTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 350 TTCTCTATCTGGGGGCTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 409
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 DB 410 CAGGCTCCGAGAGACTTTTCAAGGGGGGCCCCCAACTGGGGCCGCTTGTAGCCCTTCTT 469
 QY 301 CTCTTTGGGGGCTGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
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 QY 361 CAACTGACAGAGT 420
 DB 530 CAACTGACAGAGT 589
 QY 421 AGTGGGGGCTGGGGGAGATTACAGCTGTATATACGGGGGCTGTGTGTGTGTGTGTGTGTGT 480
 DB 590 AGTGGGGGCTGGGGGAGATTACAGCTGTATATACGGGGGCTGTGTGTGTGTGTGTGTGTGT 649
 QY 481 CGTCTGGGGGAGGGGAACTGGGCACTCACTGAGAGACAGTGTGTGTGTGTGTGTGTGTGT 540
 DB 650 CGTCTGGGGGAGGGGAACTGGGCACTCACTGAGAGACAGTGTGTGTGTGTGTGTGTGTGT 709
 QY 541 GGGGGCCCTGT 582
 DB 710 GGGGGCCCTGT 751

RESULT 11
 LOCUS BC074021 3545 bp mRNA linear ROD 30-JUN-2004
 DEFINITION Rattus norvegicus cDNA clone MGC:91704 IMAGE:7105621, complete cds.
 ACCESSION BC074021
 VERSION BC074021.1 GI:49256646
 KEYWORDS MGC.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 1 (bases 1 to 3545)
 Strausberg, R.L., Fengold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenman, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Bietow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.D., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Datchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Urdin, T.B., Tomshilsky, S., Carninci, P., Prange, C., Saha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McEwen, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Moxley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W., Vallat, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Heaton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE
 JOURNAL
 PUBLISHED
 12/7/932
 2 (bases 1 to 3545)
 Strausberg, R.
 Direct Submission
 Submitted (23-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2530, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Howard Jacobs
 cDNA Library Preparation: Express Genomics
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
 Gaithersburg, Maryland
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nsl.nih.gov
 Akhtar, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Maserian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stancitop, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggin, L., Young, A., Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
 Series: IRAC Plate: 175 Row: P Column: 4
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11177885.
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 /query Match 90.5%; Score 527.6; DB 10; Length 3545;
 Best Local Similarity 94.2%; Pred. No. 9e-109;
 Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 ORIGIN
 QY 1 ATGGGAGACCCAGGCTGGGCCCCAGACACAGGGGCTGTGNGGAGACTTTGATGTTAT 60
 DB 170 ATGGGAGACCCAGGCTGGGCCCCAGACACAGGGGCTGTGNGGAGACTTTGATGTTAT 229
 QY 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGAGGGCCAGAGCTGAC 120
 DB 230 AAGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGAGGGCCAGAGCTGAC 289
 QY 121 CCGCTGACCAAGCCATGCGGGGAGCTGGAGATGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 290 CCGCTGACCAAGCCATGCGGGGAGCTGGAGATGATGATGATGATGATGATGATGATGATGATGAT 349
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 DB 350 TTCTCTATCTGGGGGCTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 409
 QY 241 CAGGCTCCGAGAGACTTTTCAAGGGGGGCCCCCAACTGGGGCCGCTTGTAGCCCTTCTT 300
 DB 410 CAGGCTCCGAGAGACTTTTCAAGGGGGGCCCCCAACTGGGGCCGCTTGTAGCCCTTCTT 469
 QY 301 CTCTTTGGGGGCTGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
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 DB 530 CAACTGACAGAGT 589
 QY 421 AGTGGGGGCTGGGGGAGATTACAGCTGTATATACGGGGGCTGTGTGTGTGTGTGTGTGTGT 480
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 DB 710 GGGGGCCCTGT 751

QY 181 TTCTGATCTGCGGCTCAGCTGATGATGACCCAGGCTCAGCCACGACCAAGCTTCAAC 240
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QY 541 GGGGCCCTGATCTGATGAGGGGCTTTTGTGCTAGCAAGTGA 582
DB 739 GGGGCCCTGATCTGATGAGGGGCTTTTGTGCTAGCAAGTGA 780

RESULT 12

AR020779 579 bp DNA linear PAT 05-DEC-1998
LOCUS AR020779
DEFINITION Sequence 1 from patent US 5789201.
ACCESSION AR020779
VERSION AR020779.1 GI:3975394

KEYWORDS Unknown.
SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 579)

AUTHORS Guastella,J.

TITLE Genes coding for bcl-2 family bcl-2 homologue

JOURNAL Patent: US 5789201-A 1 04-AUG-1998;

FEATURES Location/Qualifiers

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/organism="unknown"

ORIGIN /mol_type="unassigned DNA"

Query Match 89.7%; Score 523; DB 6; Length 579;

Best Local Similarity 94.0%; Pred. No. 1.2e-107;

Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGGACCCAGGCTCGGCCCCAGACACACAGGCTCTGTGAGAGCTTTGATGATTAT 60
DB 1 ATGGGACCCAGGCTCGGCCCCAGACACACAGGCTCTGTGAGAGCTTTGATGATTAT 60
QY 61 AAGCTGAGAGAGAGGTTATGTCTGTGAGAGCTGGCCCGGGAGAGGCCCCAGACGCTGAC 120
DB 61 AAGCTGAGAGAGAGGTTATGTCTGTGAGAGCTGGCCCGGGAGAGGCCCCAGACGCTGAC 120
QY 121 CCGGTGACCAAGCAATGCGGGAGCTGTGAGATGATTTGAGACCCGCTTCCGGCCGAC 180
DB 121 CCGGTGACCAAGCAATGCGGGAGCTGTGAGATGATTTGAGACCCGCTTCCGGCCGAC 180
QY 181 TTCTGATCTGCGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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QY 241 CAGGCTCTCGAGCAATCTTTTCAAGGGGGCCCAACCTGGGGCCGCTGTGACCTTCTT 300
DB 241 CAGGCTCTCGAGCAATCTTTTCAAGGGGGCCCAACCTGGGGCCGCTGTGACCTTCTT 300

QY 301 CTCTTTGGGGGCTGCACTGCTGTGAGAGTGTCAACAAAGAGATGAAACAATGCTGGGA 360
DB 301 GTCTTTGGGGGCTGCTGCTGTGAGAGTGTCAACAAAGAGATGAAACAATGCTGGGA 360
QY 361 CAGGCTCTCGAGCAATCTTTTCAAGGGGGCCCAACCTGGGGCCGCTGTGACCTTCTT 420
DB 361 CAGGCTCTCGAGCAATCTTTTCAAGGGGGCCCAACCTGGGGCCGCTGTGACCTTCTT 420
QY 421 AGTGGGGGCTGCGGAGGTTTCAAGCTGTATACGGGGAACGGGGCCCTGGAGAGGCGCG 480
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DB 481 CGTCTGCGGAGGAGGAACTGGGCACTGATGAGAGCAATGCTGACGGGGGCTGTGGCACTG 540
QY 541 GGGGCCCTGATCTGATGAGGGGCTTTTGTGCTAGCAAG 579
DB 541 GGGGCCCTGATCTGATGAGGGGCTTTTGTGCTAGCAAG 579

RESULT 13

MMU59746 582 bp mRNA linear ROD 29-SEP-1996
LOCUS MMU59746
DEFINITION Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION U59746
VERSION U59746.1 GI:1572494

KEYWORDS Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 582)

AUTHORS Jenkins,N.A.,

TITLE Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,

Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.

bcl-w, a novel member of the bcl-2 family, promotes cell survival

Oncogene 13 (4), 665-675 (1996)

96358615

8761287

2 (bases 1 to 582)

Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and

Cory,S.

Direct Submission

Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and

Eliza Hall Institute of Medical Research, PO Royal Melbourne

Hospital, Parkville, Victoria 3050, Australia

Location/Qualifiers

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/gene="bcl-w"

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/note="Promotes cell survival; Bcl-2 homologue"

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GAALCAESVVKEMEPVGVQVDMVAIVLEIRLADWTHSSGWAFFTALYGDALBEAR

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FEATURES
source

Query Match 89.7%; Score 522.8; DB 10; Length 582;

Best Local Similarity 93.6%; Pred. No. 1.4e-107;

Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

ORIGIN

QY 1 ATGGGACCCAGGCTCGGCCCCAGACACACAGGCTCTGTGAGAGCTTTGATGATTAT 60

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|-----------------------|---|-----------|
| | /gene="Bcl-w" | |
| | /number=2 | |
| exon | 171. .610 | |
| | /gene="Bcl-w" | |
| | /number=3 | |
| CDS | 179. .760 | |
| | /gene="Bcl-w" | |
| | /codon_start=1 | |
| | /product="BCL-W" | |
| | /protein_id="AA866430.1" | |
| | /db_xref="GI:2623250" | |
| | /translation="MATPASTPTPTALVADPNVGYKLRQKYVYCGAGPGEPPADPLHQ | |
| | AMRPADEFEFRFRKFTSDLAQDLHTPGSAQGRFTQVSEBLTQGGPNMRLLVAFVFE | |
| | GALICASVKNEMEPVLGVQVQDMVVALLETRLADWLHS SGGMAEFTALYGDGLAEAR | |
| | RLREGMASVRTVLVTGAVLGLAVTGAFPAASK" | |
| | 611. .3476 | |
| | /gene="Bcl-w" | |
| | /number=4 | |
| | 3356. .3364 | |
| | /gene="Bcl-w" | |
| | /note="mRNA destabilization element" | |
| | 3428. .3441 | |
| | /gene="Bcl-w" | |
| ORIGIN | | |
| polyA_signal | | |
| Query Match | 89.7%; Score 522.8; DB 10; Length 3476; | |
| Best Local Similarity | 93.6%; Pred. No. 1,1e-107; | |
| Matches | 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0; | |
| OY | 1 ATGGCGACCCAGCCTTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT | 60 |
| Db | 179 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT | 238 |
| OY | 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCAGCAGCTGAC | 120 |
| Db | 239 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCTGGGAGGAGCCAGCCGCGAC | 298 |
| OY | 121 CCGCTGACACCAAGCCATGCGGGGAGCTGAGATGAGTTTCAGAACCCGCTTCGGCGCAC | 180 |
| Db | 299 CCGTGCACCAAGGCATGCGGGGCTGCGAGAGGAGTTTGAAGCCGTTTCCGCGCAC | 358 |
| OY | 181 TTCTCTGATCTGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTCAAC | 240 |
| Db | 359 TTCTCTGACCTGCGCGCTCAGCTACGTAACCCAGGCTCAGCCAGCAACGCTTCAAC | 418 |
| OY | 241 CAGGCTTCGCCAGCACTTTTTCAAAGGGGGCCCAACTGGGGCGGCTTGTAGCTTTT | 300 |
| Db | 419 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTTAACTGGGGCGGCTTGTAGCACTTT | 478 |
| OY | 301 CTCTTTGGGGGCTGACCTGTGTGCTGAGAGGTCAACAAGAGAGATGAAACCACTGGTGGGA | 360 |
| Db | 479 GTCTTTGGGGGCTGCGCTGTGTGTGCTGAGAGGTCAACAAGAAATGAGCCTTTGTGGGGA | 538 |
| OY | 361 CAAGTGCAGAGTGTGATGTGGCCCTTACCTGGAAGACGGGGCTGTGACTGATTCACAGC | 420 |
| Db | 539 CAAATGCAGAGTTGTGATGTGGCCTTACCTGGAAGACAGTGTGGCTGACTGATTCACAGC | 598 |
| OY | 421 AGTGGGGGCTGGGGTGGAGTTCAACAGCTCTATACGGGGAACGGGGCCCTGGAGAGAGCGCGG | 480 |
| Db | 599 AGTGGGGGCTGGGGGCGGAGTTCAACAGCTCTATACGGGGGAACGGGGCCCTGGAGAGAGCAGG | 658 |
| OY | 481 CGTCTGCGGAGGAGGAACTGAGGCATCAGTAGAGGACAGTGTCTGACGAGGGGCGGTGTGCACTG | 540 |
| Db | 659 CGTCTGCGGAGGAGGAACTGGGCATCAGTAGAGGACAGTGTCTGACGAGGGGCGGTGTGCACTG | 718 |
| OY | 541 GGGGCGCTGTGTAAGTGTAGGGGCGCTTTTGTCTAGCAAGTGA | 582 |
| Db | 719 GGGGCGCTGTGTAAGTGTAGGGGCGCTTTTGTCTAGCAAGTGA | 760 |

AK172925 3442 bp mRNA linear ROD 28-JUL-2004
LOCUS AK172925
DEFINITION Mus musculus mRNA for mKIAA0271 protein.
ACCESSION AK172925
VERSION AK172925.1 GI:50510434
KEYWORDS FLI_CDNA.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Okazaki, N., Kikuno, R.F., Ohara, R., Inamoto, S., Koseki, H., Kikawa, S., Suga, Y., Sano, S., Nishimura, M., Kaiho, T., Hoshino, K., Kitamura, H., Nagase, T., Ohara, O. and Koga, H.
TITLE Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries
JOURNAL DNA Res. 11, 205-218 (2004)
REFERENCE 2
AUTHORS Okazaki, N., Kikuno, R.F., Nagase, T., Ohara, O. and Koga, H.
TITLE Direct Submission
JOURNAL Submitted (19-MAY-2004) Hiasashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics; 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:mousekazusa.or.jp; Tel:81-438-52-3919; Fax:81-438-52-3918)
COMMENT The CREATE program supported by Japan science and technology corporation; cDNA full insert sequencing; Kazusa DNA Research Institute; cDNA library construction, clone selection and 5'- & 3'-end one pass sequencing.
FEATURES
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1..3442
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="m1a06063"
/note="vector:modified pBC SK+"
1..3442
/gene="mKIAA0271"
1..581
/gene="mKIAA0271"
/note="CDS is predicted by in silico analysis. Start codon is not identified."
/evidence="not experimental"
/product="mKIAA0271 protein"
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/db_xref="GI:50510435"
/translation="RMAPASTPDPTRALVADPVGKLRQGVVCGAGPGEAPADPLH QAMRAQDEFEFRFRFTSDLAALHVTGPSAQORFTQVSDLFQGGPMMGRVAFV FGAALCAESVNMEMPVGVQDDMVAVYLETRLADWIIHSSGMAEFTALYGDALSEA RLRREGNMAVSTVLTGLNVALGALVTGAFPC"
ORIGIN
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Best Local Similarity 93.5%; Pred. No. 3.3e-105;
Matches 545; Conservative 0; Mismatches 37; Indels 1; Gaps 1;
QY 1 ATGGGACCCCGAGCTTGGCGCCCGACAGACACGCGGCTCTGGTGCGAGACTTTGAGGTTAT 60
DB 6 ATGGCGACCCCGAGCTTGGCGCCCGACAGACACGCGGCTCTGGTGCGAGACTTTGAGGTTAT 65
QY 61 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCGCCCGGGAGGGGCCAGAGAGCTGAC 120
DB 66 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCGCCCGGGAGGGGCCAGAGAGCTGAC 125
QY 121 CCGCTGACACCAAGCCATGCGGGGAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCACC 180
DB 126 CCGCTGACACCAAGCCATGCGGGGAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCACC 185
QY 181 TTCTCTGATTTGGCGGCTGACGTGACATGACCCCAAGGCTCAAGCCAGCAAGCTTCACC 240
DB 186 TTCTCTGACCTGGCCGCTGAGTACAGTACCCCAAGGCTCAAGCCAGCAAGCTTCACC 245

QY 241 CAGGTCTCCGACGAACTTTTTCAGGGGCCCCCACTGGGGCCGCTTGTAGCTTTCTT 300
DB 246 CAGGTTCCGACGAACTTTTTCAGGGGCCCCCACTGGGGCCGCTTGTAGCTTTCTT 305
QY 301 CTCTTTGGGCGTGCAGCTGTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGTGGGA 360
DB 306 GTCTTTGGGCGTGCAGCTGTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGTGGGA 365
QY 361 CAGTGCAGAGTGTGATGTGGCTTACCTGAGAGACGGGCTGTGACATGATCCACAGC 420
DB 366 CAGTGCAGAGTGTGATGTGGCTTACCTGAGAGACGGGCTGTGACATGATCCACAGC 425
QY 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATAAGGGAGCGGGCCCTGAGAGAGCGCG 480
DB 426 AGTGGGGCTGGCGGAGTTCAAGCTCTATAAGGGAGCGGGCCCTGAGAGAGCGCG 485
QY 481 CGTCTGGGAGGGGAACTGGGCATCACTGAGAGACAGTGTCTGACGGGGCCGTGGCACTG 540
DB 486 CGTCTGGGAGGGGAACTGGGCATCACTGAGAGACAGTGTCTGACGGGGCCGTGGCACTG 545
QY 541 GGGGCCCTGTATCTGTAGGGGCC-TTTTGTCTAGCAAGTGA 582
DB 546 GGGGCCCTGTATCTGTAGGGGCC-TTTTGTCTAGCAAGTGA 588

Search completed: April 10, 2005, 18:37:53
Job time : 3078.26 secs

CC family, extracted from an adult brain library. This gene promotes cell

QY 481 CGCTGCGGAGGAGAACTGGGATCATGATGAGACAGTGTGACGCGGGGCGGTGCACTG 540
DB 481 CGTTCGCGGAGGAGAACTGGGATCATGATGAGACAGTGTGACGCGGGGCGGTGCACTG 540
QY 541 GGGGCGCTGTGTAATCTGTAGGGGCTTTTGTGTCAGCAAGTGA 583
DB 541 GGGGCGCTGTGTAATCTGTAGGGGCTTTTGTGTCAGCAAGTGA 583
RESULT 3
ABV78153
ID ABV78153 standard; DNA; 582 BP.
XX
AC ABV78153;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human bcl-2 DNA SEQ ID NO 37.
XX
DE RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;
XX
KM virucide; protozoacide; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200255693-A2.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2002; 2002MO-EP000152.
XX
PR 09-JAN-2001; 2001DE-01000586.
PR 26-OCT-2001; 2001DE-01055280.
PR 29-NOV-2001; 2001DE-01058411.
PR 07-DEC-2001; 2001DE-01060151.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Lämmer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-590671/63.
XX
PT Inhibiting expression of target gene, useful e.g. for inhibiting
XX
PT oncogenes, by administering double-stranded RNA complementary to the
XX
PT target and having an overhang.
XX
PS Claim 10; Page 134; 203pp; German.
XX
XX
CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA is complementary to (I) and at least one end of dsRNA
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in Plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention
XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;
Query Match 99.0%; Score 577.2; DB 6; Length 582;
Best Local Similarity 99.5%; Pred. No. 2.8e-134;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGCGACCCCGAGCTGCGGCCCGACACACGCGGCTCGTGGTGAGACTTTGTAGTTAT 60
DB 1 ATGGCGACCCCGAGCTGCGGCCCGACACACGCGGCTCGTGGTGAGACTTTGTAGTTAT 60
QY 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGCGGCCCGGAGGAGGCGCAGCAGCTGAC 120
DB 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGCGGCCCGGAGGAGGCGCAGCAGCTGAC 120

QY 121 CGGCTGACCAAGCAATGCGGGGAGCTGAGATGATGAGACCCGCTTCCGGCGCACC 180
DB 121 CGGCTGACCAAGCAATGCGGGGAGCTGAGATGATGAGACCCGCTTCCGGCGCACC 180
QY 181 TTCTGTATCTGAGCGGCTCAGCTGATGTGATGACCCAGGCTCAGCCAGCAACGTTGACC 240
DB 181 TTCTGTATCTGAGCGGCTCAGCTGATGTGATGACCCAGGCTCAGCCAGCAACGTTGACC 240
QY 241 CAGGCTCCGAGCAACTTTTCAAGGGGGGCCCACTGCGGGCGCTTGTAGCTTTCTT 300
DB 241 CAGGCTCCGAGCAACTTTTCAAGGGGGGCCCACTGCGGGCGCTTGTAGCTTTCTT 300
QY 301 CTCTTTGGGGCTGCACTGTGTGTGAGAGTGAACAGAGATGGAACCACTGTGTGGA 360
DB 301 GTCTTTGGGGCTGCACTGTGTGTGAGAGTGAACAGAGATGGAACCACTGTGTGGA 360
QY 361 CAAGTCAGAGATGATGTGTGCTTACCTTGAGACCGGCGCTGTGATTCACAGC 420
DB 361 CAAGTCAGAGATGATGTGTGCTTACCTTGAGACCGGCGCTGTGATTCACAGC 420
QY 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATACGGGAGCGGGCCCTGAGAGGCGCGG 480
DB 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATACGGGAGCGGGCCCTGAGAGGCGCGG 480
QY 481 CGTCTGCGGGAGGGGAACTGGGATCATGATGAGACAGTGTGACGGGGGCGTGGCACTG 540
DB 481 CGTCTGCGGGAGGGGAACTGGGATCATGATGAGACAGTGTGACGGGGGCGTGGCACTG 540
QY 541 GGGGCGCTGTGTAATCTGTAGGGGCTTTTGTGTCAGCAAGTGA 582
DB 541 GGGGCGCTGTGTAATCTGTAGGGGCTTTTGTGTCAGCAAGTGA 582
RESULT 4
ABZ35729
ID ABZ35729 standard; DNA; 582 BP.
XX
AC ABZ35729;
XX
DT 07-FEB-2003 (first entry)
XX
DE Human bcl-2 polynucleotide SEQ ID NO 37.
XX
XX
KM Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
KM protozoacide; gene expression; antisense; tumour; infection; Plasmodium;
KM virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
KM Hepatitis C virus; human papilloma virus; gene; ds.
XX
OS Homo sapiens.
XX
PN DE10100588-A1.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2001; 2001DE-01000588.
XX
PR 09-JAN-2001; 2001DE-01000588.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Lämmer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-683450/74.
XX
PT Inhibiting expression of target genes, useful e.g. for treating tumors,
XX
PT by introducing into cells two double-stranded RNAs that are complementary
XX
XX
PS Claim 13; Page 30-31; 100pp; German.
XX
CC The invention relates to inhibiting expression of a target gene in a cell
CC by introducing at least two oligonucleotides (dsRNA and II), both

CC a catalytic domain, binding domains contiguous with the 5' and 3' end of
CC the catalytic domain, and therefore hybridises with, the two regions
CC immediately flanking the purine residue of the cleavage site within the
CC bcl-2 gene family mRNA, at which DNazyme-catalysed cleavage is desired. A
CC pharmacetic composition comprising a DNazyme of the invention is
CC useful for treating tumours in a subject, and for enhancing the
CC sensitivity of malignant or virus infected cells infected cells to
CC therapy. The DNazymes are useful in diagnostics, therapeutics,
CC prophylaxis, research agents and in kits. The DNazymes are also useful
CC for increasing the susceptibility of tumour cells to anti-tumour
CC therapies such as chemotherapy and radiation therapy. This polynucleotide
CC sequence represents a human bcl-2 gene of the invention
CX

Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;

| | | | | |
|-----------------------|--------------|---------------------|---------------|--------------|
| Query Match | 98.6%; | Score 575; | DB 8; | Length 3542; |
| Best Local Similarity | 99.1%; | Pred. No. 1.5e-133; | | |
| Matches 578; | Conservative | 0; | Mismatches 5; | Indels 0. |

| | | | |
|----|-----|---|-----|
| QY | 1 | ATGGCGACCCCAAGCTTGGGCCCCAGACACACGSGGCTTGGTGGCAGACTTTGAGTTAT | 60 |
| Db | 177 | ATGGCGACCCCAAGCTTGGGCCCCAGACACACGSGGCTTGGTGGCAGACTTTGAGTTAT | 236 |
| QY | 61 | AAGCTAGGCGAAGGGTTATGTCTGGAGCTGGGCCCGGGGAGGGGCCACAGCTGAC | 120 |
| Db | 237 | AAGCTAGGCGAAGGGTTATGTCTGGAGCTGGGCCCGGGGAGGGGCCACAGCTGAC | 296 |
| QY | 121 | CCGCTGACCAAGCCATGCGGGCAGCTGGAGATGATTCAGAACCCGCTTCCGGGCGAC | 180 |
| Db | 297 | CCGCTGACCAAGCCATGCGGGCAGCTGGAGATGATTCAGAACCCGCTTCCGGGCGAC | 356 |
| QY | 181 | TTCTCGATCTGGCCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCATTAC | 240 |
| Db | 357 | TTCTCGATCTGGCCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCATTAC | 416 |
| QY | 241 | CAGGTCCTCCAGCACTTTTCAAGGGGGCCCCAATGGGGGCGGCTGTAGCTTCTT | 300 |
| Db | 417 | CAGGTCCTCCAGCACTTTTCAAGGGGGCCCCAATGGGGGCGGCTGTAGCTTCTT | 476 |
| QY | 301 | CTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAGAGATGAACCACTGGTGGGA | 360 |
| Db | 477 | CTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAGAGATGAACCACTGGTGGGA | 536 |
| QY | 361 | CAAGTCAGAGAGTGGATGTTGGCCCTAATTGGAGAGCGGGCTGTGACTGATTCACAGC | 420 |
| Db | 537 | CAAGTCAGAGAGTGGATGTTGGCCCTAATTGGAGAGCGGGCTGTGACTGATTCACAGC | 596 |
| QY | 421 | AGTGGGGGCTGGCGGAGTTCAAGCTCTATACGGGGACGGGGGCTGGAGAGAGCGCGG | 480 |
| Db | 597 | AGTGGGGGCTGGCGGAGTTCAAGCTCTATACGGGGACGGGGGCTGGAGAGAGCGCGG | 656 |
| QY | 481 | CGTCTGCGGGAGGGGAACTGGGCATCAGTGAAGACAAGTGTCAAGGGGGCGTGGCACTG | 540 |
| Db | 657 | CGTCTGCGGGAGGGGAACTGGGCATCAGTGAAGACAAGTGTCAAGGGGGCGTGGCACTG | 716 |
| QY | 541 | GGGGCCCTGGTAACTGATAGGGGCGCTTTTGTCTAGCAAGTGA 583 | |
| Db | 717 | GGGGCCCTGGTAACTGATAGGGGCGCTTTTGTCTAGCAAGTGA 759 | |

```

RESULT 8
AAAX25132
ID      AAAX25132  standard; DNA; 581 BP
XX

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| | |
|----|--|
| AC | AAx25132; |
| XX | |
| XX | 05-JUL-1999 (first entry) |
| DT | |
| XX | |
| DE | Human bcl-w gene. |
| XX | |
| XX | |
| KW | Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility; |
| XX | animal model; ss. |
| XX | |

OS Homo sapiens.
XX
PN W09913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
XX WPI; 1999-243890/20.
DR P-PSDB; AAY05530.
XX
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.
XX
XX
PS Claim 3; Page 32; 52pp; English.

line present sequence is the human bcl-w gene encoding Bcl-w protein (see AAY05530), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation in at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganized seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other;

| | | | | |
|-----------------------|--------------|---------------------|---------------|-------------------|
| Query Match | 98.3% | Score 573; | DB 2; | length 581; |
| Best Local Similarity | 99.1%; | Pred. No. 3.2e-133; | | |
| Matches 576; | Conservative | 0; | Mismatches 5; | Indels 0; Gaps 0. |

| | | | |
|----|-----|--|-----|
| QY | 1 | ATGGCAACCCAGCTCGAGCCCCAGACAACAAGGGCTCTGGTGGCAACTTTTGTAGTTAT | 60 |
| Db | 1 | ATGGCAACCCAGCTCGAGCCCCAGACAACAAGGGCTCTGGTGGCAACTTTTGTAGTTAT | 60 |
| QY | 61 | AAGCTGAGGCAGAGAGGTTATGTCTGTGAGACTGAGCCCGAGGAGGGCCACAGACTGAC | 120 |
| Db | 61 | AAGCTGAGGCAGAGAGGTTATGTCTGTGAGACTGAGCCCGAGGAGGGCCACAGACTGAC | 120 |
| QY | 121 | CGGCTGCACCAAGCCATGCGGGACGCTGAGATGATTTGAAACCGCTTCCGGGGCACCC | 180 |
| Db | 121 | CGGCTGCACCAAGCCATGCGGGACGCTGAGATGATTTGAAACCGCTTCCGGGGCACCC | 180 |
| QY | 181 | TTCTCTGATCTGGGGGCTCAGCTGCATGTGATACCCAGCTCAGGCCACGAAACGTTTCAAC | 240 |
| Db | 181 | TTCTCTGATCTGGGGGCTCAGCTGCATGTGATACCCAGCTCAGGCCACGAAACGTTTCAAC | 240 |
| QY | 241 | CAGGCTCTCCGACGAATTTTTCAAGGGGGGCCCAACTGAGGGCCGCTTGTAGCTTCTTT | 300 |
| Db | 241 | CAGGCTCTCCGATGAACTTTTCAAGGGGGGCCCAACTGAGGGCCGCTTGTAGCTTCTTT | 300 |
| QY | 301 | CTCTTTGGGGGTGCACTGTGTGCTGAGAGTGTTCACCAAGAGATGTGAACCACTGGTGGGA | 360 |
| Db | 301 | GTCTTTGGGGGTGCACTGTGTGCTGAGAGTGTTCACCAAGAGAGATGTGAACCACTGGTGGGA | 360 |
| QY | 361 | CAAGTGACAGAGTGTGATGTGTGCTTACCTTGAGAGACGCGGCTGTGTGCACTGGATTCACAGC | 420 |
| Db | 361 | CAAGTGACAGAGTGTGATGTGTGCTTACCTTGAGAGACGCGGCTGTGTGCACTGGATTCACAGC | 420 |
| QY | 421 | AGTGGGGGCTGGGGCGGAGTTCAACGCTCTATTCGGGGAGCGGGGCCCTTGAGAGAGACCGCG | 480 |

61 AAGCTGAGGCAGAGGGTTATGTTCTGTGGAGCTGGCCCCGGGGAGGGCCAGCAGCTGAC 120

XX

[illegible]

Db 481 CGCTGCGGGAGGGCAACTGGGCATGAGTGAACACAGTGGTGAACGGGGCCGTGGCACTG 540

QY 541 GGGGCCCTGGTAACTGTAGGGGCCCTTTTGTCTAGCAAGTG 581

Db 541 GGGGCCCTGGTAACTGTAGGGGCCCTTTTGTCTAGCAAGTG 581

Search completed: April 10, 2005, 16:55:35
Job time : 462.785 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 16:31:16 ; Search time 144.247 Seconds
(without alignments)
6613.285 Million cell updates/sec

Title: US-09-925-674B-6

Perfect score: 583

Sequence: 1 atggcgacccagcagctgcgc.....cttttcgtcagcaagtgaa 583

Scoring table: IDENTITY_NUC

Gap 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | # Query Match | Length | ID | Description |
|------------|-------|---------------|--------|----------------------|--------------------|
| 1 | 583 | 100.0 | 583 | US-09-155-327G-6 | Sequence 6, Appli |
| 2 | 572.4 | 98.2 | 582 | US-09-949-016-5057 | Sequence 5057, Ap |
| 3 | 567.8 | 97.4 | 579 | US-08-798-897-2 | Sequence 2, Appli |
| 4 | 567.8 | 97.4 | 579 | US-08-978-523-2 | Sequence 2, Appli |
| 5 | 523 | 89.7 | 579 | US-08-978-897-1 | Sequence 1, Appli |
| 6 | 523 | 89.7 | 579 | US-08-978-523-1 | Sequence 1, Appli |
| 7 | 501 | 85.9 | 581 | US-09-155-327G-8 | Sequence 8, Appli |
| 8 | 424 | 72.7 | 1098 | US-09-010-147B-23 | Sequence 23, Appli |
| 9 | 423.6 | 72.7 | 1864 | US-09-149-476-130 | Sequence 130, App |
| 10 | 423.4 | 72.6 | 5199 | US-09-949-016-16799 | Sequence 16799, A |
| 11 | 414.6 | 71.1 | 601 | US-09-949-016-177003 | Sequence 177003, |
| 12 | 131 | 22.5 | 926 | US-08-081-448-5 | Sequence 5, Appli |
| 13 | 131 | 22.5 | 926 | US-08-470-670A-6 | Sequence 6, Appli |
| 14 | 131 | 22.5 | 926 | US-08-481-739-1 | Sequence 1, Appli |
| 15 | 131 | 22.5 | 926 | US-09-167-921-1 | Sequence 1, Appli |
| 16 | 131 | 22.5 | 926 | US-09-277-020-39 | Sequence 39, Appli |
| 17 | 131 | 22.5 | 926 | US-09-323-743-1 | Sequence 1, Appli |
| 18 | 131 | 22.5 | 926 | US-08-461-511A-6 | Sequence 1, Appli |
| 19 | 131 | 22.5 | 926 | US-09-271-014A-5 | Sequence 5, Appli |
| 20 | 131 | 22.5 | 926 | US-09-023-655-1430 | Sequence 1430, Ap |
| 21 | 131 | 22.5 | 926 | US-09-814-915A-106 | Sequence 106, App |
| 22 | 131 | 22.5 | 926 | PCT-US94-07089-6 | Sequence 6, Appli |
| 23 | 131 | 22.5 | 1236 | US-09-639-245-1 | Sequence 1, Appli |
| 24 | 127.6 | 21.9 | 1455 | US-09-639-245-7 | Sequence 7, Appli |
| 25 | 125 | 21.4 | 711 | US-09-741-238-1 | Sequence 1, Appli |
| 26 | 123.4 | 21.2 | 717 | US-08-465-485A-20 | Sequence 20, Appli |
| 27 | 123.4 | 21.2 | 717 | US-09-080-285-20 | Sequence 20, Appli |

| | | | | | | |
|----|-------|------|-------|---|---------------------|--------------------|
| 28 | 123.4 | 21.2 | 4825 | 6 | 5459251-1 | Patent No. 5459251 |
| 29 | 123.4 | 21.2 | 4825 | 6 | 5459251-1 | Patent No. 5459251 |
| 30 | 123.4 | 21.2 | 5086 | 2 | US-08-465-485A-19 | Sequence 19, Appli |
| 31 | 123.4 | 21.2 | 5086 | 2 | US-08-365-486A-14 | Sequence 14, Appli |
| 32 | 123.4 | 21.2 | 5086 | 3 | US-09-080-285-19 | Sequence 19, Appli |
| 33 | 123.4 | 21.2 | 5086 | 3 | US-08-880-342-14 | Sequence 14, Appli |
| 34 | 123.4 | 21.2 | 5086 | 3 | US-09-724-426-19 | Sequence 19, Appli |
| 35 | 123.4 | 21.2 | 5086 | 3 | US-09-233-527-7 | Sequence 7, Appli |
| 36 | 123.4 | 21.2 | 5086 | 5 | PCT-US93-06251-4 | Sequence 4, Appli |
| 37 | 123.4 | 21.2 | 5086 | 5 | PCT-US93-06251-2 | Sequence 2, Appli |
| 38 | 123.4 | 21.2 | 5094 | 3 | US-09-234-186-7 | Sequence 7, Appli |
| 39 | 123.4 | 21.2 | 5104 | 6 | 5506344-1 | Patent No. 5506344 |
| 40 | 123.4 | 21.2 | 5104 | 6 | 5506344-1 | Patent No. 5506344 |
| 41 | 123.2 | 21.1 | 60489 | 4 | US-09-949-016-16287 | Sequence 16287, A |
| 42 | 121.8 | 20.9 | 760 | 4 | US-08-405-702A-11 | Sequence 11, Appli |
| 43 | 121.8 | 20.9 | 6030 | 4 | US-09-023-655-1015 | Sequence 1015, Ap |
| 44 | 120.4 | 20.7 | 1384 | 4 | US-08-899-367-1 | Sequence 1, Appli |
| 45 | 120.2 | 20.6 | 1846 | 2 | US-08-365-486A-16 | Sequence 16, Appli |

ALIGNMENTS

| | | |
|---|--------------------------------------|------------------|
| RESULT 1 | US-09-155-327G-6 | US-09-155-327G-6 |
| Sequence 6, Application US/09155327G | | |
| Patent No. 6790637 | | |
| GENERAL INFORMATION: | | |
| APPLICANT: AMRAD Operations Pty Ltd | | |
| TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2 | | |
| TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES | | |
| FILE REFERENCE: 2096584 | | |
| CURRENT APPLICATION NUMBER: US/09/155.327G | | |
| CURRENT FILING DATE: 1999-03-29 | | |
| PRIOR APPLICATION NUMBER: PM8965 | | |
| PRIOR FILING DATE: 1996-03-27 | | |
| NUMBER OF SEQ ID NOS: 15 | | |
| SOFTWARE: Patentin Ver. 2.1 | | |
| SEQ ID NO 6 | | |
| LENGTH: 583 | | |
| TYPE: DNA | | |
| ORGANISM: HUMAN | | |
| FEATURE: | | |
| NAME/KEY: CDS | | |
| LOCATION: (1)..(579) | | |
| US-09-155-327G-6 | | |
| Query Match | 100.0%; Score 583; DB 4; Length 583; | |
| Best Local Similarity | 100.0%; Pred. No. 1.7e-144; | |
| Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| QY 1 ATGGCGACCCAGCCTGCGGCCCGACACACAGGCGCTGTGTGCGACACTTTGATGTTAT 60 | | |
| Db 1 ATGGCGACCCAGCCTGCGGCCCGACACACAGGCGCTGTGTGCGACACTTTGATGTTAT 60 | | |
| QY 61 AAGTGAAGGAGAGGTTATGCTGTGAGCTGCGCCCGGAGAGGCGCCAGCAGCTGAC 120 | | |
| Db 61 AAGTGAAGGAGAGGTTATGCTGTGAGCTGCGCCCGGAGAGGCGCCAGCAGCTGAC 120 | | |
| QY 121 CCGTGACCAAGCATGCGGAGAGTGAAGATGATTCAGACCCGCTTCGGCGCACC 180 | | |
| Db 121 CCGTGACCAAGCATGCGGAGAGTGAAGATGATTCAGACCCGCTTCGGCGCACC 180 | | |
| QY 181 TTCTGTATGTGGGGCTGACGTGATGTGACCCAGGCTCAGCCAGCAGCTTACC 240 | | |
| Db 181 TTCTGTATGTGGGGCTGACGTGATGTGACCCAGGCTCAGCCAGCAGCTTACC 240 | | |
| QY 241 CAGTCTCCGACGAATTTTCAAGGGGGCCCACTGGGGCGCTTGAGCTTTT 300 | | |
| Db 241 CAGTCTCCGACGAATTTTCAAGGGGGCCCACTGGGGCGCTTGAGCTTTT 300 | | |
| QY 301 CTCCTTGGGCTGCACTGTGTGTGAGAGTGTCAACAGAGATGAAACCACTGTGTGGA 360 | | |
| Db 301 CTCCTTGGGCTGCACTGTGTGTGAGAGTGTCAACAGAGATGAAACCACTGTGTGGA 360 | | |

Db 301 CTCCTTTGGGCTGCACTGTGTGCTGAGAGTTCACAGAGATGGAACCACTGTGGGA 360
QY 361 CAAGTGAGAGATGATGTGTGCTTACCTTGAGACCGGCTGTGTGATGATCCAGAC 420
Db 361 CAAGTGAGAGATGATGTGTGCTTACCTTGAGACCGGCTGTGTGATGATCCAGAC 420
QY 421 AGTGGGGGCTGGCGGAGTTTCAAGCTTATACGGGGACGGGGCTTGAAGAGCGCGG 480
Db 421 AGTGGGGGCTGGCGGAGTTTCAAGCTTATACGGGGACGGGGCTTGAAGAGCGCGG 480
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Db 481 CGTCTGGGGAGAGGGAACCTGGGCATCATAGTGAAGACAGTGTGAGCGGGCCGTGCACTG 540
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Db 541 GGGGCTCTGTACTGTAGTGGGCTTTTGTGTAGCAAGTGA 583

RESULT 2

US-09-949-016-5057
Sequence 5057, Application US/09949016
Patent No. 6812319
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949, 016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5057
LENGTH: 582
TYPE: DNA
ORGANISM: Human
US-09-949-016-5057

Query Match 98.2%; Score 572.4; DB 4; Length 582;
Best Local Similarity 99.0%; Pred. No. 1.1e-141;
Matches 576; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGGCAACCCAGCTCCGCCCCCAGACACACGGGCTGTGTGAGACCTTGTAGTTAT 60
Db 1 ATGGGCAACCCAGCTCCGCCCCCAGACACACGGGCTGTGTGAGACCTTGTAGTTAT 60
QY 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGCCCCGGGGAGGGCCCAAGCTGAC 120
Db 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGCCCCGGGGAGGGCCCAAGCTGAC 120
QY 121 CCGCTGACCAAGCAGATGCGGCGCTGAGATGATGTTGAGACCCGCTTCCGGCCACC 180
Db 121 CCACTGACCAAGCAGATGCGGCGCTGAGATGATGTTGAGACCCGCTTCCGGCCACC 180
QY 181 TTCTCTGATCTGCGGCTGAGCTCATGTGACCCCAAGGCTCAACCAAGCTTCAAC 240
Db 181 TTCTCTGATCTGCGGCTGAGCTCATGTGACCCCAAGGCTCAACCAAGCTTCAAC 240
QY 241 CAGGCTCCCAAGAACTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTACCTTTCTT 300
Db 241 CAGGCTCCCAAGAACTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTACCTTTCTT 300
QY 301 CTCCTTTGGGCTGCACTGTGTGCTGAGAGTGAACAAGAGATGGAACCACTGTGGGA 360
Db 301 CTCCTTTGGGCTGCACTGTGTGCTGAGAGTGAACAAGAGATGGAACCACTGTGGGA 360
QY 361 CAAGTGAGAGATGATGTGTGCTTACCTTGAGACCGGCTGTGTGATGATCCAGAC 420

Db 361 CAAGTGAGAGATGATGTGTGCTTACCTTGAGACCGGCTGTGTGATGATCCAGAC 420
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Db 421 AGTGGGGGCTGGCGGAGTTTCAAGCTTATACGGGGACGGGGCTTGAAGAGCGCGG 480
QY 481 CGTCTGGGGAGAGGGAACCTGGGCATCATAGTGAAGACAGTGTGAGCGGGCCGTGCACTG 540
Db 481 CGTCTGGGGAGAGGGAACCTGGGCATCATAGTGAAGACAGTGTGAGCGGGCCGTGCACTG 540
QY 541 GGGGCTCTGTACTGTAGTGGGCTTTTGTGTAGCAAGTGA 582
Db 541 GGGGCTCTGTACTGTAGTGGGCTTTTGTGTAGCAAGTGA 582

RESULT 3

US-08-798-897-2
Sequence 2, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-1, a Bcl-2
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798, 897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ramond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483, 0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-798-897-2

Query Match 97.4%; Score 567.8; DB 1; Length 579;
Best Local Similarity 98.8%; Pred. No. 1.8e-140;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGGCAACCCAGCTCCGCCCCCAGACACACGGGCTGTGTGAGACCTTGTAGTTAT 60
Db 1 ATGGGCAACCCAGCTCCGCCCCCAGACACACGGGCTGTGTGAGACCTTGTAGTTAT 60
QY 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGCCCCGGGGAGGGCCCAAGCTGAC 120
Db 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGCCCCGGGGAGGGCCCAAGCTGAC 120
QY 121 CCGCTGACCAAGCAGATGCGGCGCTGAGATGATGTTGAGACCCGCTTCCGGCCACC 180
Db 121 CCACTGACCAAGCAGATGCGGCGCTGAGATGATGTTGAGACCCGCTTCCGGCCACC 180

Qy 181 TTCTGTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
Db 181 TTCTGTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
Qy 241 CAGGCTTCGACGAACTTTTCAAGGGGGCCCAACTGGGGCCCGCTTGTAGCTTCTTT 300
Db 241 CAGGCTTCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCCCGCTTGTAGCTTCTTT 300
Qy 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGAGATGGAACCACTGTGGGA 360
Db 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGAGATGGAACCACTGTGGGA 360
Qy 361 CAAGTCAGAGATGATGTGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 CAAGTCAGAGATGATGTGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 421 AGTGGGGCTGGGGCGAGATTCAACAGCTTATACGGGGACGGGGCCCTGAGAGAGAGAGAG 480
Db 421 AGTGGGGCTGGGGCGAGATTCAACAGCTTATACGGGGACGGGGCCCTGAGAGAGAGAGAG 480
Qy 481 CGTCTGCGGAG 540
Db 481 CGTCTGCGGAG 540
Qy 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGTAGCAAG 579
Db 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGTAGCAAG 579

RESULT 4
US-08-978-523-2
Sequence 2, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Gene Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Emond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483,0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-08-978-523-2

Query Match 97.4%; Score 567.8; DB 2; Length 579;
Best Local Similarity 98.8%; Pred. No. 1.8e-140;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ATGCGAACCCAGGCTCGGCCCCAGACACAGGCTCTGTGTGAGACATTTGTAGATTAT 60
Db 1 ATGCGAACCCAGGCTCGGCCCCAGACACAGGCTCTGTGTGAGACATTTGTAGATTAT 60
Qy 61 AAGCTGAGGCAAGAGGTTATGTCTGTGAGCTTGGCCCCGGGGAGGGGCCAGAGCTTAC 120
Db 61 AAGCTGAGGCAAGAGGTTATGTCTGTGAGCTTGGCCCCGGGGAGGGGCCAGAGCTTAC 120
Qy 121 CCGCTGACCAAGCATGCGGGGAGCTGAGATGATGATGAGACCGCTTCCGGGAGC 180
Db 121 CCACTGACCAAGCATGCGGGGAGCTGAGATGATGATGAGACCGCTTCCGGGAGC 180
Qy 181 TTCTGTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
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Db 241 CAGGCTTCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCCCGCTTGTAGCTTCTTT 300
Qy 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGAGATGGAACCACTGTGGGA 360
Db 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGAGATGGAACCACTGTGGGA 360
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Db 361 CAAGTCAGAGATGATGTGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
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Db 481 CGTCTGCGGAG 540
Qy 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGTAGCAAG 579
Db 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGTAGCAAG 579

RESULT 5
US-08-798-897-1
Sequence 1, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Gene Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Emond, Robert W.

REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-798-897-1

Query Match 89.7%; Score 523; DB 1; Length 579;
Best Local Similarity 94.0%; Pred. No. 1,2e-128;
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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QY 1 ATGGGAGACCCGACCTCGGCCCCAGACACACGCGGCTGTGTGAGAGATTAT 60
DB 1 ATGGGAGACCCGACCTCGGCCCCAGACACACGCGGCTGTGTGAGAGATTAT 60
QY 61 AAGCTGAGACAGAGAGGTTATGTCTGTGAGAGTGGCCCCGGGAGAGGCCCAAGCTGAC 120
DB 61 AAGCTGAGACAGAGAGGTTATGTCTGTGAGAGTGGCCCCGGGAGAGGCCCAAGCTGAC 120
QY 121 CCGCTGACCAAGGCAATGCGGGGCACTGAGAGATGTTGAGACCCGCTTCCGGGCGAC 180
DB 121 CCGCTGACCAAGGCAATGCGGGGCACTGAGAGATGTTGAGACCCGCTTCCGGGCGAC 180
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QY 301 CTCTTTGGGGCTCAGCTGTGTGTGAGAGTGTGATGATGATGATGATGATGATGATGAT 360
DB 301 CTCTTTGGGGCTCAGCTGTGTGTGAGAGTGTGATGATGATGATGATGATGATGATGAT 360
QY 361 CAAGTGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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QY 421 AGTGGGGGCTGGGCGGAGTTCAAGCTCTATACCGGGGAGCGGGGCTTGGAGAGCGCGG 480
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QY 541 GGGGCGCTGTGATCTGTAGGGGCTTTTGTCTGCAAG 579
DB 541 GGGGCGCTGTGATCTGTAGGGGCTTTTGTCTGCAAG 579
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RESULT 6
US-08-978-523-1

Sequence 1, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-978-523-1

Query Match 89.7%; Score 523; DB 2; Length 579;
Best Local Similarity 94.0%; Pred. No. 1,2e-128;
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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QY 1 ATGGGAGACCCGACCTCGGCCCCAGACACACGCGGCTGTGTGAGAGATTAT 60
DB 1 ATGGGAGACCCGACCTCGGCCCCAGACACACGCGGCTGTGTGAGAGATTAT 60
QY 61 AAGCTGAGACAGAGAGGTTATGTCTGTGAGAGTGGCCCCGGGAGAGGCCCAAGCTGAC 120
DB 61 AAGCTGAGACAGAGAGGTTATGTCTGTGAGAGTGGCCCCGGGAGAGGCCCAAGCTGAC 120
QY 121 CCGCTGACCAAGGCAATGCGGGGCACTGAGAGATGTTGAGACCCGCTTCCGGGCGAC 180
DB 121 CCGCTGACCAAGGCAATGCGGGGCACTGAGAGATGTTGAGACCCGCTTCCGGGCGAC 180
QY 181 TTCTGTGATCTGCGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
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QY 241 CAGGTCTCCAGCAATCTTTTCAAGGGGGCCCCAAGCTGGGGCGGCTTGTAGCTTTCTT 300
DB 241 CAGGTCTCCAGCAATCTTTTCAAGGGGGCCCCAAGCTGGGGCGGCTTGTAGCTTTCTT 300
QY 301 CTCTTTGGGGCTCAGCTGTGTGTGAGAGTGTGATGATGATGATGATGATGATGATGAT 360
DB 301 CTCTTTGGGGCTCAGCTGTGTGTGAGAGTGTGATGATGATGATGATGATGATGATGAT 360
QY 361 CAAGTGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 CAAGTGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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DB 421 AGTGGGGGCTGGGCGGAGTTCAAGCTCTATACCGGGGAGCGGGGCTTGGAGAGCGCGG 480
QY 481 CGTCTGCGGAGAGGGAATGCGGCATGATGAGAGCAAGTGTGACGCGGGGCGTGTGACATG 540
DB 481 CGTCTGCGGAGAGGGAATGCGGCATGATGAGAGCAAGTGTGACGCGGGGCGTGTGACATG 540
QY 541 GGGGCGCTGTGATCTGTAGGGGCTTTTGTCTGCAAG 579
DB 541 GGGGCGCTGTGATCTGTAGGGGCTTTTGTCTGCAAG 579
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Db 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAG 579

RESULT 7
US-09-155-327G-8
Sequence 8, Application US/09155327G
Patent No. 6790637
GENERAL INFORMATION:
APPLICANT: AMRAD Operations Pty Ltd
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
FILE REFERENCE: 2096584
CURRENT APPLICATION NUMBER: US/09/155.327G
CURRENT FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: P8965
PRIOR FILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 8
LENGTH: 581
TYPE: DNA
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(579)
US-09-155-327G-8

Query Match 85.9%; Score 501; DB 4; Length 581;
Best Local Similarity 91.4%; Pred. No. 8e-123;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 1 ATGCGACCCAGGCTGGCCCGACAGACAGGCGCTCTGGGAGACTTTGATGTTAT 60
Db 1 ATGCGACCCAGGCTGGCCCGACAGACAGGCGCTCTGGGAGACTTTGATGTTAT 60
Qy 61 AAGCTGAGGAGAGAGGTTATGTCGTGAGAGCTGAGCCCGGGAGAGGCGCCAGAGCTGAC 120
Db 61 AAGCTGAGGAGAGAGGTTATGTCGTGAGAGCTGAGCCCGGGAGAGGCGCCAGAGCTGAC 120
Qy 121 CCGCTGACCAAGCCATGCGGGAGCTGAGAGATGATGAGACCCGCTTCGGCGCAC 180
Db 121 CCGCTGACCAAGCCATGCGGGAGCTGAGAGATGATGAGACCCGCTTCGGCGCAC 180
Qy 181 TTCTCTGATCTGGGCGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 181 TTCTCTGATCTGGGCGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
Qy 181 TTCTCTGATCTGGGCGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 181 TTCTCTGATCTGGGCGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
Qy 241 CAGGCTCCGACGAATTTTTCAGAGGGGCGCCAACTGAGGCGCGCTTGTAGCTTCTT 300
Db 241 CAGGCTCCGACGAATTTTTCAGAGGGGCGCCAACTGAGGCGCGCTTGTAGCTTCTT 300
Qy 301 GTCTTTGGGCGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Db 301 GTCTTTGGGCGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Qy 361 CAGGTGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 CAGGTGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy 421 AGTGGGAGTGGGCGAGTTCACAGCTTATACGGGAGCGGGCGCTTGTAGCTTCTT 480
Db 421 AGTGGGAGTGGGCGAGTTCACAGCTTATACGGGAGCGGGCGCTTGTAGCTTCTT 480
Qy 481 CGTGTGCGGAGGCGCACTGGGCACTGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 CGTGTGCGGAGGCGCACTGGGCACTGATGATGATGATGATGATGATGATGATGATGATGAT 540
Qy 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGT 581
Db 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGT 581

RESULT 8

US-09-010-147B-23
Sequence 23, Application US/09010147B
Patent No. 6653445
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: Human Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.147B
FILING DATE: 12-Jan-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-Jan-1997
APPLICATION NUMBER: US 60/034,204
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: P353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1095
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-010-147B-23

Query Match 72.7%; Score 424; DB 4; Length 1098;
Best Local Similarity 98.8%; Pred. No. 2.2e-102;
Matches 427; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGCGACCCAGGCTGGCCCGACAGACAGGCGCTCTGGGAGACTTTGATGTTAT 60
Db 1 ATGCGACCCAGGCTGGCCCGACAGACAGGCGCTCTGGGAGACTTTGATGTTAT 60
Qy 61 AAGCTGAGGAGAGAGGTTATGTCGTGAGAGCTGAGCCCGGGAGAGGCGCCAGAGCTGAC 120
Db 61 AAGCTGAGGAGAGAGGTTATGTCGTGAGAGCTGAGCCCGGGAGAGGCGCCAGAGCTGAC 120
Qy 121 CCGCTGACCAAGCCATGCGGGAGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 180
Db 121 CCGCTGACCAAGCCATGCGGGAGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 180
Qy 181 TTCTCTGATCTGGGCGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 181 TTCTCTGATCTGGGCGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Qy 241 CAGGCTCCGACGAATTTTTCAGAGGGGCGCCAACTGAGGCGCGCTTGTAGCTTCTT 300
Db 241 CAGGCTCCGACGAATTTTTCAGAGGGGCGCCAACTGAGGCGCGCTTGTAGCTTCTT 300

us-09-925-674b-6.rn1

| | | | |
|----|-----|---|-----|
| OY | 301 | CTCTTTGGGGCTGCACGCTGTCTGAGAGTTCACAAAGAGATGAAACCACTGGTGGG | 367 |
| Db | 301 | GCTTTTGGGCTGCACGTGTGTGAGAGTTCACAAAGAGATGAAACCACTGTTGGG | 367 |
| OY | 361 | CAAGTCAGAGAGTGATGTGTGGCTTACCTGAGACGCGGCTGTGCACTGATCCACAGC | 420 |
| Db | 361 | CAAGTCAGAGAGTGATGTGTGGCTTACCTGAGAGACGCGGCTGTGCACTGATCCACAGC | 420 |
| OY | 421 | AGTGGGGGCTGG | 432 |
| Db | 421 | AGTGGGGGCTGG | 432 |

Sequence 130, Application US/09145476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P200221
CITING REFERENCE:

CURRENT APPLICATION NUMBER: US/09/149,476
EARLIER FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/040,336
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EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
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EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23

| | |
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| 1 | EARLIER APPLICATION NUMBER: 60/047, 582 |
| 2 | EARLIER FILING DATE: 1997-05-23 |
| 3 | EARLIER APPLICATION NUMBER: 60/047, 596 |
| 4 | EARLIER FILING DATE: 1997-05-23 |
| 5 | EARLIER APPLICATION NUMBER: 60/047, 612 |
| 6 | EARLIER FILING DATE: 1997-05-23 |
| 7 | EARLIER APPLICATION NUMBER: 60/047, 632 |
| 8 | EARLIER FILING DATE: 1997-05-23 |
| 9 | EARLIER APPLICATION NUMBER: 60/047, 601 |
| 10 | EARLIER FILING DATE: 1997-05-23 |
| 11 | EARLIER APPLICATION NUMBER: 60/043, 580 |
| 12 | EARLIER FILING DATE: 1997-04-11 |
| 13 | EARLIER APPLICATION NUMBER: 60/043, 568 |
| 14 | EARLIER FILING DATE: 1997-04-11 |
| 15 | EARLIER APPLICATION NUMBER: 60/043, 314 |
| 16 | EARLIER FILING DATE: 1997-04-11 |
| 17 | EARLIER APPLICATION NUMBER: 60/043, 569 |
| 18 | EARLIER FILING DATE: 1997-04-11 |
| 19 | EARLIER APPLICATION NUMBER: 60/043, 311 |
| 20 | EARLIER FILING DATE: 1997-04-11 |
| 21 | EARLIER APPLICATION NUMBER: 60/043, 671 |
| 22 | EARLIER FILING DATE: 1997-04-11 |
| 23 | EARLIER APPLICATION NUMBER: 60/043, 674 |
| 24 | EARLIER FILING DATE: 1997-04-11 |
| 25 | EARLIER APPLICATION NUMBER: 60/043, 669 |
| 26 | EARLIER FILING DATE: 1997-04-11 |
| 27 | EARLIER APPLICATION NUMBER: 60/043, 312 |
| 28 | EARLIER FILING DATE: 1997-04-11 |
| 29 | EARLIER APPLICATION NUMBER: 60/043, 313 |
| 30 | EARLIER FILING DATE: 1997-04-11 |
| 31 | EARLIER APPLICATION NUMBER: 60/043, 672 |
| 32 | EARLIER FILING DATE: 1997-04-11 |
| 33 | EARLIER APPLICATION NUMBER: 60/043, 315 |
| 34 | EARLIER FILING DATE: 1997-04-11 |
| 35 | EARLIER APPLICATION NUMBER: 60/048, 974 |
| 36 | EARLIER FILING DATE: 1997-05-06 |
| 37 | EARLIER APPLICATION NUMBER: 60/056, 886 |
| 38 | EARLIER FILING DATE: 1997-08-22 |
| 39 | EARLIER APPLICATION NUMBER: 60/056, 877 |
| 40 | EARLIER FILING DATE: 1997-08-22 |
| 41 | EARLIER APPLICATION NUMBER: 60/056, 889 |
| 42 | EARLIER FILING DATE: 1997-08-22 |
| 43 | EARLIER APPLICATION NUMBER: 60/056, 893 |
| 44 | EARLIER FILING DATE: 1997-08-22 |
| 45 | EARLIER APPLICATION NUMBER: 60/056, 630 |
| 46 | EARLIER FILING DATE: 1997-08-22 |
| 47 | EARLIER APPLICATION NUMBER: 60/056, 878 |
| 48 | EARLIER FILING DATE: 1997-08-22 |
| 49 | EARLIER APPLICATION NUMBER: 60/056, 662 |
| 50 | EARLIER FILING DATE: 1997-08-22 |
| 51 | EARLIER APPLICATION NUMBER: 60/056, 872 |
| 52 | EARLIER FILING DATE: 1997-08-22 |
| 53 | EARLIER APPLICATION NUMBER: 60/056, 882 |
| 54 | EARLIER FILING DATE: 1997-08-22 |
| 55 | EARLIER APPLICATION NUMBER: 60/056, 637 |
| 56 | EARLIER FILING DATE: 1997-08-22 |
| 57 | EARLIER APPLICATION NUMBER: 60/056, 903 |
| 58 | EARLIER FILING DATE: 1997-08-22 |
| 59 | EARLIER APPLICATION NUMBER: 60/056, 888 |
| 60 | EARLIER FILING DATE: 1997-08-22 |
| 61 | EARLIER APPLICATION NUMBER: 60/056, 879 |
| 62 | EARLIER FILING DATE: 1997-08-22 |
| 63 | EARLIER APPLICATION NUMBER: 60/056, 880 |
| 64 | EARLIER FILING DATE: 1997-08-22 |
| 65 | EARLIER APPLICATION NUMBER: 60/056, 894 |
| 66 | EARLIER FILING DATE: 1997-08-22 |
| 67 | EARLIER APPLICATION NUMBER: 60/056, 911 |
| 68 | EARLIER FILING DATE: 1997-08-22 |
| 69 | EARLIER APPLICATION NUMBER: 60/056, 636 |
| 70 | EARLIER FILING DATE: 1997-08-22 |
| 71 | EARLIER APPLICATION NUMBER: 60/056, 874 |
| 72 | EARLIER FILING DATE: 1997-08-22 |
| 73 | EARLIER APPLICATION NUMBER: 60/056, 910 |

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EARLIER APPLICATION NUMBER: 60/056, 864
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EARLIER APPLICATION NUMBER: 60/056, 892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057, 761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047, 595
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 594
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EARLIER APPLICATION NUMBER: 60/047, 593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043, 578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047, 501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043, 670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056, 632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048, 964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057, 650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056, 884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057, 669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049, 610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061, 060
EARLIER FILING DATE: 1997-10-02

Query Match 72.7%; Score 423.6; DB 3; Length 1864;
Best Local Similarity 98.6%; Pred. No. 3.3e-102;
Matches 426; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGGACCCCAAGCTGGCCCGGAGACACCGGCTGTGAGGACCTTTAGTTAT 60
DB 11 ATGGGACCCCAAGCTGGCCCGGAGACACCGGCTGTGAGGACCTTTAGTTAT 70
QY 61 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCCCGGAGGAGCCAGCAGCTGAC 120
DB 71 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCCCGGAGGAGCCAGCAGCTGAC 130
QY 121 CCGCTGACCAAGCATTGCGGCGAGCTGAGATGATTTGAGACCCCGTTCCGCGCAC 180
DB 131 CCGCTGACCAAGCATTGCGGCGAGCTGAGATGATTTGAGACCCCGTTCCGCGCAC 190
QY 181 TTCTGATCTGGGGCTGACGCTGAGTACCCCAAGCTCAGCCAGCAAGCTTAC 240
DB 191 TTCTGATCTGGGGCTGACGCTGAGTACCCCAAGCTCAGCCAGCAAGCTTAC 250
QY 241 CAGGCTCCGACGAACTTTTCAAGGGGCGCCCACTGGGGCGCTTGTAGCTTCTT 300
DB 251 CAGGCTCCGACGAACTTTTCAAGGGGCGCCCACTGGGGCGCTTGTAGCTTCTT 310
QY 301 CTCTTGGGCTGACCTGTGTCTGAGAGTGTCAACAGAGATGAACTGTGGGA 360
DB 311 GTCTTGGGCTGACCTGTGTCTGAGAGTGTCAACAGAGATGAACTGTGGGA 370
QY 361 CAAGTGAGAGTGTGAGTGTGCTTACTGAGACCGGGCTGTGCTGATTCAGAC 420
DB 371 CAAGTGAGAGTGTGAGTGTGCTTACTGAGACCGGGCTGTGCTGATTCAGAC 430
QY 421 AGTGGGGGCTGG 432
DB 431 AGTGGGGGCTGG 442

RESULT 10
US-09-949-016-16799
Sequence 16799, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16799
LENGTH: 5199
TYPE: DNA
ORGANISM: Human
US-09-949-016-16799

Query Match 72.6%; Score 423.4; DB 4; Length 5199;
Best Local Similarity 98.6%; Pred. No. 5.3e-102;
Matches 427; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGGGACCCCAAGCTGGCCCGGAGACACCGGCTGTGAGGACCTTTAGTTAT 60
DB 2001 ATGGGACCCCAAGCTGGCCCGGAGACACCGGCTGTGAGGACCTTTAGTTAT 2060
QY 61 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCCCGGAGGAGCCAGCAGCTGAC 120
DB 2061 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCCCGGAGGAGCCAGCAGCTGAC 2120
QY 121 CCGCTGACCAAGCATTGCGGCGAGCTGAGATGATTTGAGACCCCGTTCCGCGCAC 180

Db 2121 CCACTGACCAAGCCATGCGGAGCTGAGATGAGTTGAGACCCCGCTTCCGCGCACC 2180
QY 181 TTCTCGATCTGGGGGCTCAGTGTGATGTGACCCCAAGGCTTAGCCAGCAACGGTTGACC 240
Db 2181 TTCTGTGATCTGGCGGCTCAGTGTGATGTGACCCCAAGGCTTAGCCAGCAACGGTTGACC 2240
QY 241 CAGGTCTCGACGAACCTTTTCAAGGGGGGCCCAACTGGGGCGCGCTTGTAGCCTTTT 300
Db 2241 CAGGTCTCGACGAACCTTTTCAAGGGGGGCCCAACTGGGGCGCGCTTGTAGCCTTTT 2300
QY 301 CTCTTTGGGGGCTGACCTGTGCTGCTGAGAGTGTCAACAAGAGATGAGAACCACTGTGGGA 360
Db 2301 GTCTTTGGGGGCTGACCTGTGCTGCTGAGAGTGTCAACAAGAGATGAGAACCACTGTGGGA 2360
QY 361 CAACTGACGAGAGTGTGAGTGTGCTTACCTGAGACCGCGGCTGTGCACTGTGATCCACAGC 420
Db 2361 CAACTGACGAGAGTGTGAGTGTGCTTACCTGAGACCGCGGCTGTGCACTGTGATCCACAGC 2420
QY 421 AGTGGGGGCTGGG 433
Db 2421 AGTGGGGGCTGGG 2433

RESULT 11
US-09-949-016-177003
; Sequence 177003, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177003
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-177003

Query Match 71.1%; Score 414.6; DB 4; Length 601;
Best Local Similarity 98.6%; Pred. No. 5.4e-100;
Matches 417; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATGGGACCCCAAGCTTGGGCCCCCAGACACACAGGGCTGTGTGGGAGACTTTGATGATTAT 60
Db 179 ATGGGACCCCAAGCTTGGGCCCCCAGACACACAGGGCTGTGTGGGAGACTTTGATGATTAT 238
QY 61 AAGCTGAGGCAAGAGGTTATGTCTGTGAGACTGCGCCCGGGAGAGGGCCCAAGAGCTGAC 120
Db 239 AAGCTGAGGCAAGAGGTTATGTCTGTGAGACTGCGCCCGGGAGAGGGCCCAAGAGCTGAC 298
QY 121 CCGGTGACCAAGCAATGCGGGCAGCTGAGATGAGTTTGAAGACCCGCTTCCGGCCACAC 180
Db 299 CCGGTGACCAAGCAATGCGGGCAGCTGAGATGAGTTTGAAGACCCGCTTCCGGCCACAC 358
QY 181 TTCTGTATCTGGGCTCAGCTGTGATGTGACCCCAAGGCTTACCCAGCAAGCTTCAACC 240
Db 359 TTCTGTATCTGGGCTCAGCTGTGATGTGACCCCAAGGCTTACCCAGCAAGCTTCAACC 418
QY 241 CAGGTCTCGACGAACCTTTTCAAGGGGGGCCCAACTGGGGCGCGCTTGTAGCCTTTT 300
Db 419 CAGGTCTCGACGAACCTTTTCAAGGGGGGCCCAACTGGGGCGCGCTTGTAGCCTTTT 478
QY 301 CTCTTTGGGGGCTGACCTGTGCTGCTGAGAGTGTCAACAAGAGATGAGAACCACTGTGGGA 360

Db 479 GTCTTTGGGGGCTGACCTGTGCTGCTGAGAGTGTCAACAAGAGATGAGAACCACTGTGGGA 538
QY 361 CAACTGACGAGAGTGTGATGTGCTTACCTGAGACCGCGGCTGTGCACTGTGATCCACAGC 420
Db 539 CAACTGACGAGAGTGTGATGTGCTTACCTGAGACCGCGGCTGTGCACTGTGATCCACAGC 598
QY 421 AGT 423
Db 599 AGT 601

RESULT 12
US-08-081-448-5
; Sequence 5, Application US/08081448
; Patent No. 5646008
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5646008th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,448
; FILING DATE: 19930622
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646008thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
US-08-081-448-5

Query Match 22.5%; Score 131; DB 1; Length 926;
Best Local Similarity 56.3%; Pred. No. 5.3e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;
QY 98 CCGGGAGGGGCCCAAGCACTGACCCCGCTGACCAAGCCATGCGGAGCTGAGATGAGT 157
Db 364 CCGGGAGGGTGATCCCATGGCAGCAAGTAAGCAAGCGCTGAGAGGAGGAGGAGCAAGT 423
QY 158 TCGAGACCCCGCTTCCCGGCGCAACCTTCTGTATGTGGGGGCTCAGCTGTGATGAGCCAG 217
Db 424 TTGAATCGGGTACCGGGCGGCAATTGAGCACTGACATTCACAGCTCACATCAACCCAG 483
QY 218 GCTCAGCCCAAGCAAGCTTCAACCCAGAGTCTCGAGCAACCTTTTCAAGGGGGGCCCAACT 277
Db 484 GACAGCATATCAGAGCTTTGAACAGGTATGATGATTAATCTTCCGGGATGGGTAACCT 543

MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-481-739-1

Query Match 22.5%; Score 131; DB 3; Length 926;
Best Local Similarity 56.3%; Pred. No. 5.3e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGGCCCAAGAGCTGACCCGCTGACCAAGCCATGCGGAGCTGAGATGAGT 157
DB 364 CCGGGAGGGATGATCCCGATGAGCAAGTAAAGCAAGCGCTGAGGAGGAGGAGCAAGT 423
QY 158 TCGAGACCCGCTTCCGGGCACTTCTGATCTGCGGGCTGAGCTGATGAGATGAGT 217
DB 424 TTGAACCTGCGGTACCGGCGGCAATTCAGTGACCTGACATCCAGCTCCACATACCCCA 483
QY 218 GCTCAGCCCAAGCAAGCTTCAAGCTTCCGAGCTTCCGAGCAAGCTTTTCAAGGGGCCCCAACT 277
DB 484 GGAACACATATCAGACCTTTGAAACAGATGATGATGATGATGATGATGATGATGATGAT 543
QY 278 GGGGCGCCCTTGTAGCTTCTTCTTGTGGGGCTGACATGCTGAGATGATGATGATGATGAT 337
DB 544 GGGGTGCAATGTGGCTTTTCTTCTTGTGGGGCTGACATGCTGAGATGATGATGATGATGAT 603
QY 338 AGGAGATGAAACCACTGTGTGAGCAAGTGCAGAGATGATGATGATGATGATGATGATGATGAT 397
DB 604 AGGAGATGCAAGTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
QY 398 GGGTGTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 457
DB 664 ACCTAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 723
QY 458 ACGGGGCGCTGAGAGGCGCGCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 517
DB 724 ACAATGCAAGAGCGGAGAGCGGAGAGCGGAGAGCGGAGAGCGGAGAGCGGAGAGCGGAGAG 783
QY 518 TGCTGACGGGGGCGG 532
DB 784 GCATGACTGTGGCG 798

RESULT 15
US-09-167-921-1
Sequence 1, Application US/09167921A
Patent No. 6172216
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, Qingling
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0324
CURRENT APPLICATION NUMBER: US/09/167, 921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1

Query Match 22.5%; Score 131; DB 3; Length 926;
Best Local Similarity 56.3%; Pred. No. 5.3e-25;

Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;
QY 98 CCGGGAGGGCCCAAGAGCTGACCCGCTGACCAAGCCATGCGGAGCTGAGATGAGT 157
DB 364 CCGGGAGGGATGATCCCGATGAGCAAGTAAAGCAAGCGCTGAGGAGGAGGAGCAAGT 423
QY 158 TCGAGACCCGCTTCCGGGCACTTCTGATCTGCGGGCTGAGCTGATGAGATGAGT 217
DB 424 TTGAACCTGCGGTACCGGCGGCAATTCAGTGACCTGACATCCAGCTCCACATACCCCA 483
QY 218 GCTCAGCCCAAGCAAGCTTCAAGCTTCCGAGCTTCCGAGCAAGCTTTTCAAGGGGCCCCAACT 277
DB 484 GGAACACATATCAGACCTTTGAAACAGATGATGATGATGATGATGATGATGATGATGAT 543
QY 278 GGGGCGCCCTTGTAGCTTCTTCTTGTGGGGCTGACATGCTGAGATGATGATGATGATGAT 337
DB 544 GGGGTGCAATGTGGCTTTTCTTCTTGTGGGGCTGACATGCTGAGATGATGATGATGATGAT 603
QY 338 AGGAGATGAAACCACTGTGTGAGCAAGTGCAGAGATGATGATGATGATGATGATGATGATGAT 397
DB 604 AGGAGATGCAAGTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
QY 398 GGGTGTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 457
DB 664 ACCTAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 723
QY 458 ACGGGGCGCTGAGAGGCGCGCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 517
DB 724 ACAATGCAAGAGCGGAGAGCGGAGAGCGGAGAGCGGAGAGCGGAGAGCGGAGAGCGGAGAG 783
QY 518 TGCTGACGGGGGCGG 532
DB 784 GCATGACTGTGGCG 798

Search completed: April 10, 2005, 20:17:21
Job time: 146.247 secs

Query Match 99.2%; Score 578.2; DB 9; Length 583;
 Best Local Similarity 99.5%; Pred. No. 1.2e-156;
 Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      : 1 ATGGCCAGCCCCAGGCTGGGCCCCAGACACAGGGGCTCTGTCGCGCAGATTGTAGTAT 60
DB      1 ATGGCCAGCCCCAGGCTGGGCCCCAGACACAGGGGCTCTGTCGCGCAGATTGTAGTAT 60
  
```

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        61 AAGCTGAGCAGAAAGGTTATGTCGTGTGAGCTGGACCCCGGGAGAGGCTCAGACGCTTAC 120
        Db AAGCTGAGCAGAAAGGTTATGTCGTGTGAGCTGGACCCCGGGAGAGGCTCAGACGCTTAC 120
        Oy 121 CCGCTGCACCAAGCCATGCGGCGAGCTGGAGATGAGTTGAGACCCCGCTTCCGCGCAC 180
        Db 121 CCGCTGCACCAAGCCATGCGGCGAGCTGGAGATGAGTTGAGACCCCGCTTCCGCGCAC 180
        Oy 181 TTCTCTGATCTGAGCGGCTTCAGCTGCATGTGACCCCAAGGCTCAGCCAGACCAAGCTTCACC 240
        Db 181 TTCTCTGATCTGAGCGGCTTCAGCTGCATGTGACCCCAAGGCTCAGCCAGACCAAGCTTCACC 240
        Oy 241 CAGGCTCTCGACGAACCTTTTCAAGGGGGGCCCAACTGAGGCGCGCTTGAGCCCTTCTTT 300
        Db 241 CAGGCTCTCGACGAACCTTTTCAAGGGGGGCCCAACTGAGGCGCGCTTGAGCCCTTCTTT 300
        Oy 301 CTCCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGAGATGAGAAACCACTGTGTGGA 360
        Db 301 CTCCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGAGATGAGAAACCACTGTGTGGA 360
        Oy 361 CAAGTGCAGAGATGATGTGTGGCTTCACTGTGAGACGAGGGCTGTGTGCACTGATTCACAGC 420
        Db 361 CAAGTGCAGAGATGATGTGTGGCTTCACTGTGAGACGAGGGCTGTGTGCACTGATTCACAGC 420
        Oy 421 AGTGGGGGCTGGGCGGAGTTCAACGCTCTTATACGGGAGACGGGCGCTTGAGAGAGGCGCG 480
        Db 421 AGTGGGGGCTGGGCGGAGTTCAACGCTCTTATACGGGAGACGGGCGCTTGAGAGAGGCGCG 480
        Oy 481 CGTCTGCGGAGGAGGAGCTGGGCACTGATGAGAGACAGTGTGACGGGGGCGCTGGCACTG 540
        Db 481 CGTCTGCGGAGGAGGAGCTGGGCACTGATGAGAGACAGTGTGACGGGGGCGCTGGCACTG 540
        Oy 541 GGGGCGCTGTGTAACCTGTGAGGGGCTTTTGTGCTAGCAAGTGAA 583
        Db 541 GGGGCGCTGTGTAACCTGTGAGGGGCTTTTGTGCTAGCAAGTGAA 583

RESULT 2
US-10-384-339C-37
; Sequence 37, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutze, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: bc1-w
; PATENT DOCUMENT NUMBER: US9747
; US-10-384-339C-37

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| Query Match | Score | DB | Length |
|-----------------------|--------|--------------------|-------------------|
| Best Local Similarity | 99.0%; | 577.2; | 582; |
| Matches | 99.5%; | Pred. No. 2,3e-16; | |
| Conservative | 0; | Mismatches 3; | Indels 0; Gaps 0; |

1 ATGGCAACCCCAAGCTCGAGCCCAAGACACAGGGGCTGTGAGGAGACTTTAGATT 60

Db 1 ATGGGACCCCAAGCCTTGGGCCCCAGACACAAGGGCTCTGTGTGGACAGCTTTGTAGGTTAT 60

QY 61 AAGCTGAGGCGAAGGGTTATGTCTGTGGAGCTGAGCCCGGGGGAGGGCCCAAGCATGTAC 120

Db 61 AAGCTGAGGCGAAGGGTTATGTCTGTGGAGCTGAGCCCGGGGGAGGGCCCAAGCATGTAC 120

QY 121 CCGGTGACCAAGCATTCGGGGCAGCTGTGAGATGATGTTGAGAACCCGCTTCCGGCGACC 180

Db 121 CCGGTGACCAAGCATTCGGGGCAGCTGTGAGATGATGTTGAGAACCCGCTTCCGGCGACC 180

QY 181 TTCTCTGATCTGGGGCTCAGCTGATCATGTACCCAGGCTCAGGCCAGCAAGCTTACC 240

Db 181 TTCTCTGATCTGGGGCTCAGCTGATCATGTACCCAGGCTCAGGCCAGCAAGCTTACC 240

QY 241 CAGGCTCCGACGAACTTTTTCAAAGGGGGCCCCAAGTGGGCGCCTTGTAGCCTTCTT 300

Db 241 CAGGCTCCGACGAACTTTTTCAAAGGGGGCCCCAAGTGGGCGCCTTGTAGCCTTCTT 300

QY 301 CTCTTTGGGGCTCAGTGTGTGAGAGTGAACAAGAGATGGAACAATGTGTGGGA 360

Db 301 GTCTTTGGGGCTCAGTGTGTGAGAGTGAACAAGAGATGGAACAATGTGTGGGA 360

QY 361 CAAGTGCAGAGATGTGATGTGGCTTACCTGAGAACCGCGCTGATCGAATGCCACAGC 420

Db 361 CAAGTGCAGAGATGTGATGTGGCTTACCTGAGAACCGCGCTGATCGAATGCCACAGC 420

QY 421 AGTGGGGGCTGGGGCGGAGTTCAAGCTCTAATCGGGAAAGGGGCCCTTGAAGAGGCGCG 480

Db 421 AGTGGGGGCTGGGGCGGAGTTCAAGCTCTAATCGGGAAAGGGGCCCTTGAAGAGGCGCG 480

QY 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAAGACAGTCTGACAGGGGGCGTGGCACTG 540

Db 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAAGACAGTCTGACAGGGGGCGTGGCACTG 540

QY 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTGTACCAAGTGA 582

Db 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTGTACCAAGTGA 582

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RESULT 3
US-10-479-832A-4
; Sequence 4, Application US/10479832A
; Publication No. US20050064407A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson Research Pty Ltd
; TITLE OF INVENTION: bcl-2 DNAzymes
; FILE REFERENCE: WtP13107942
; CURRENT APPLICATION NUMBER: US/10/479, 832A
; CURRENT FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-832A-4

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| Query Match | 98.2% | Score 572.4 | DB 19 | Length 582 |
|-----------------------|----------------|---|----------|------------|
| Best Local Similarity | 99.0% | Pred. No. 5.5e-155 | | |
| Matches 576 | Conservative 0 | Mismatches 6 | Indels 0 | Gaps 0 |
| QY | 1 | ATGGGACCCCGCAGCTCTGGGCCGACACACCGGGCTCTGGTGGCAACATTTGTAGGTTAT | 60 | |
| Db | 1 | ATGGGAGACCCCGAGCTCTGGGCCGACACACCGGGCTCTGGTGGCAACATTTGTAGGTTAT | 60 | |
| QY | 61 | AAGCTGAGGCGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGCCACAGCTGAC | 120 | |
| Db | 61 | AAGCTGAGGCGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGCCACAGCTGAC | 120 | |
| QY | 121 | CGGCTGACACAAAGCCATGCGGGGCGAGCTGGAGATGAATTTGAACCCGCTTTCCGGGCGACC | 180 | |
| Db | 121 | CGGCTGACACAAAGCCATGCGGGGCGAGCTGGAGATGAATTTGAACCCGCTTTCCGGGCGACC | 180 | |

QY 181 TTCTCTGATCTGGGGCTCAGCTGCATGTGACCCAGGCTGAGCCAGCAAGCTTCAAC 240
Db 181 TTCTCTATCTGGGGCTCAGCTGCATGTGACCCAGGCTGAGCCAGCAAGCTTCAAC 240
QY 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCCCTTGTAGCTTCTTT 300
Db 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCCCTTGTAGCTTCTTT 300
QY 301 CTCTTTGGGGCTGCACTGTGTGTCTGAGAGTGTCAACAAAGAGATGAAACCACTGGTGGGA 360
Db 301 GTCTTTGGGGCTGCACTGTGTGTCTGAGAGTGTCAACAAAGAGATGAAACCACTGGTGGGA 360
QY 361 CAAGTGACAGAGTGTGATGTGTGGCTTACCTGAGACGGGGCTGTGTGACTGTGATCCACAGC 420
Db 361 CAAGTGACAGAGTGTGATGTGTGGCTTACCTGAGACGGGGCTGTGTGACTGTGATCCACAGC 420
QY 421 AGTGGGGGCTGGGGGAGTTTCAAGCTCTATACGGGGACGGGGCCCTTGGAGAGGCGCG 480
Db 421 AGTGGGGGCTGGGGGAGTTTCAAGCTCTATACGGGGACGGGGCCCTTGGAGAGGCGCG 480
QY 481 CGTCTGGGGAGGGGAACTGGGATCACTGAGAGACAGTGTGACGGGGCCGTGGCACTG 540
Db 481 CGTCTGGGGAGGGGAACTGGGATCACTGAGAGACAGTGTGACGGGGCCGTGGCACTG 540
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGA 582
Db 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGA 582

RESULT 4

US-09-925-674A-8
; Sequence 8, Application US/09925674A
; Patent No. US2002011943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925, 674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925, 674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: P8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-925-674A-8

Query Match 89.1%; Score 519.6; DB 9; Length 582;

Best Local Similarity 93.3%; Pred. No. 9,1e-140;
Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGGCTGGCCCGACAGACAGGGCTCTGGTGGAGACTTTGTAGTTAT 60
Db 1 ATGGCGACCCAGGCTGGCCCGACAGACAGGGCTCTGGTGGAGACTTTGTAGTTAT 60
QY 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCAGAGCTGAC 120
Db 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCAGAGCTGAC 120
QY 121 CCGCTGACCAAGCAGCTGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGAC 180
Db 121 CCGCTGACCAAGCAGCTGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGAC 180
QY 181 TTCTCTATCTGGGGCTCAGCTGCATGTGACCCAGGCTGAGCCAGCAAGCTTCAAC 240

Db 181 TTCTCTACCTGGCGCTGAGCTACAGTACCCAGGCTCAGCCAGCAAGCTTCAAC 240
QY 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCCCTTGTAGCTTCTTT 300
Db 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCCCTTGTAGCTTCTTT 300
QY 301 CTCTTTGGGGCTGCACTGTGTGTCTGAGAGTGTCAACAAAGAGATGAAACCACTGGTGGGA 360
Db 301 GTCTTTGGGGCTGCACTGTGTGTCTGAGAGTGTCAACAAAGAGATGAAACCACTGGTGGGA 360
QY 361 CAAGTGACAGAGTGTGATGTGTGGCTTACCTGAGACGGGGCTGTGTGACTGTGATCCACAGC 420
Db 361 CAAGTGACAGAGTGTGATGTGTGGCTTACCTGAGACGGGGCTGTGTGACTGTGATCCACAGC 420
QY 421 AGTGGGGGCTGGGGGAGTTTCAAGCTCTATACGGGGACGGGGCCCTTGGAGAGGCGCG 480
Db 421 AGTGGGGGCTGGGGGAGTTTCAAGCTCTATACGGGGACGGGGCCCTTGGAGAGGCGCG 480
QY 481 CGTCTGGGGAGGGGAACTGGGATCACTGAGAGACAGTGTGACGGGGCCGTGGCACTG 540
Db 481 CGTCTGGGGAGGGGAACTGGGATCACTGAGAGACAGTGTGACGGGGCCGTGGCACTG 540
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGA 582
Db 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGA 582

RESULT 5

US-09-809-391-130
; Sequence 130, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruden et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809, 391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1648)
; OTHER INFORMATION: n equals a,t,c,g, or c
US-09-809-391-130

Query Match 72.7%; Score 423.6; DB 10; Length 1864;

Best Local Similarity 98.6%; Pred. No. 4,7e-112;
Matches 426; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGGCTGGCCCGACAGACAGGGCTCTGGTGGAGACTTTGTAGTTAT 60
Db 1 ATGGCGACCCAGGCTGGCCCGACAGACAGGGCTCTGGTGGAGACTTTGTAGTTAT 70
QY 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCAGAGCTGAC 120
Db 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCAGAGCTGAC 130
QY 121 CCGCTGACCAAGCAGCTGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGAC 180
Db 121 CCGCTGACCAAGCAGCTGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGAC 190
QY 181 TTCTCTATCTGGGGCTCAGCTGCATGTGACCCAGGCTGAGCCAGCAAGCTTCAAC 240
Db 181 TTCTCTATCTGGGGCTCAGCTGCATGTGACCCAGGCTGAGCCAGCAAGCTTCAAC 250
QY 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCCCTTGTAGCTTCTTT 300

Db 251 CAGTCTCCGATGAATTTTTCAGAGGGGCCCAACTGGGGCCGCTGTAGCTTCTTT 310
QY 301 CTCTTTGGGGCTGACGTGTCTGTGAGTGTCAACAGAGATGGAACCACTGGTGGGA 360
Db 311 GTCTTTGGGGCTGACGTGTCTGTGAGTGTCAACAGAGATGGAACCACTGGTGGGA 370
QY 361 CAGTCCAGAGATGATGTGTGGCTTACTGTGAGACGGCGCTGGTGTGATTCACACGC 420
Db 371 CAGTCCAGAGATGATGTGTGGCTTACTGTGAGACGGCGCTGGTGTGATTCACACGC 430
QY 421 AGTGGGGGGCTGG 432
Db 431 AGTGGGGGGCTGG 442

RESULT 6
US-09-882-171-130
Sequence 130, Application US/09882171
Publication No. US20030175858A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/809,391
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/038,621
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,626
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,334
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,336
PRIOR FILING DATE: 1997-03-07
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PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/047,600
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,615
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PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,502
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,633
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,583
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,617
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,618
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,503
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,592
PRIOR FILING DATE: 1997-05-23
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PRIOR FILING DATE: 1997-05-23

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PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,903
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PRIOR APPLICATION NUMBER: 60/056,911

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PRIOR APPLICATION NUMBER: 60/057,761
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PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043,670
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/056,632
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,664
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,876
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,881
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,909
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,875
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,862
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,887
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,908
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/048,964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/057,650
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/057,669
PRIOR FILING DATE: 1997-09-05
Query Match 72.7%; Score 423.6; DB 10; Length 1864;

Best Local Similarity 98.6%; Pred. No. 4,7e-112;
Matches 426; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATGGCGACCCCAAGCTTCGGCCCAAGACACACCGGCTTGTGGCAGACTTTGAGTTAT 60
Db 11 ATGGCGACCCCAAGCTTCGGCCCAAGACACACCGGCTTGTGGCAGACTTTGAGTTAT 70
QY 61 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCCCGGGAGGGCCAGAGCTGAC 120
Db 71 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCCCGGGAGGGCCAGAGCTGAC 130
QY 121 CCGCTGACCAAGACCAATGCGGAGAGTGAATGATTCAGACCCGCTTCCGGCGACC 180
Db 131 CCGCTGACCAAGACCAATGCGGAGAGTGAATGATTCAGACCCGCTTCCGGCGACC 190
QY 181 TTCTGTATGTGGGGCTCAGCTGATGTGATCCCAAGCTCAGCCAGCAAGCTTACC 240
Db 191 TTCTGTATGTGGGGCTCAGCTGATGTGATCCCAAGCTCAGCCAGCAAGCTTACC 250
QY 241 CAGGTCCGACGAACCTTTTCAAGGGGGCCCAAGTGGGGCCGCTTGTAGCTTCTTT 300
Db 251 CAGGTCCGACGAACCTTTTCAAGGGGGCCCAAGTGGGGCCGCTTGTAGCTTCTTT 310
QY 301 CTCTTGGGGCTGCACTGTGTGCTGAGAGTCAACAAGAGATGGAACCACTGTGGGA 360
Db 311 GTCTTGGGGCTGCACTGTGTGCTGAGAGTCAACAAGAGATGGAACCACTGTGGGA 370
QY 361 CAAGTCAGAGATGTGATGTGGCTTACCTGAGACCGGCTGTGCACTGATTCACAGC 420
Db 371 CAAGTCAGAGATGTGATGTGGCTTACCTGAGACCGGCTGTGCACTGATTCACAGC 430
QY 421 AAGTGGGGGCTGG 432
Db 431 AAGTGGGGGCTGG 442
RESULT 7
US-10-164-861-130
Sequence 130, Application US/10164861
Publication No. US20030225248A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 130
LENGTH: 1864
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: SITE
LOCATION: (1648)
OTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-130
Query Match 72.7%; Score 423.6; DB 17; Length 1864;
Best Local Similarity 98.6%; Pred. No. 4,7e-112;
Matches 426; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATGGCGACCCCAAGCTTCGGCCCAAGACACACCGGCTTGTGGCAGACTTTGAGTTAT 60
Db 11 ATGGCGACCCCAAGCTTCGGCCCAAGACACACCGGCTTGTGGCAGACTTTGAGTTAT 70
QY 61 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCCCGGGAGGGCCAGAGCTGAC 120
Db 71 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCCCGGGAGGGCCAGAGCTGAC 130

10-029-386-10549

```

1 Sequence 10549, Application US/10029386
2 Publication No. US20030194704A1
3 GENERAL INFORMATION:
4 APPLICANT: Penn, Sharron G.
5 APPLICANT: Rank, David R.
6 APPLICANT: Hanzel, David K.
7 TITLE OR INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEOTID
8 FILE REFERENCE: ABOMICA-X-2
9 CURRENT APPLICATION NUMBER:
10 CURRENT FILING DATE: US/10/029,386
11 NUMBER OF SEQ ID NOS: 34288
12 SOFTWARE: Annotmax Sequence Listing Engine ver6.1.1
13 SEQ ID NO 10549
14 LENGTH: 578
15 TYPE: DNA
16 ORGANISM: Homo sapiens
17 FEATURE:
18 OTHER INFORMATION: MAP TO CHR14.3
19 OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 4.2
20 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3
21 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
22 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
23 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
24 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
25 OTHER INFORMATION: NT HIT: g11475115, EVALUE 0.00e+000
26 US-10-029-386-10549
27 SWISSPROT HIT: Q92843, EVALUE 2.00e+000

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[illegible][illegible]

RESULT 9
US-10-02

Sequence 24249

```

1 Publication 24249, Application No. US10029386
2 GENERAL INFORMATION:
3 APPLICANT: Penn, Sharon G.
4 APPLICANT: Hankel, David K.
5 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEOTIDE
6 FILE REFERENCE: AEWICA-X-2
7 CURRENT APPLICATION NUMBER: US/10/029,386
8 NUMBER OF SEQ ID NOS: 34288
9 SOFTWARE: Anomax Sequence Listing Engine ver. 1.1
10 SEQ ID NO 24249
11 LENGTH: 433
12 TYPE: DNA
13 ORGANISM: Homo sapiens
14 FEATURE:
15 OTHER INFORMATION: MAP TO CHR14.3
16 OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 4.2
17 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
18 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
19 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
20 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
21 OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 0.006+0.0072
22 OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALUE 2.006-0.0072
23 US-10-029-386-24249

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Query Match

| | | | |
|----|-----|--|-----|
| | 1 | ATGGGAGACCCCAAGCTTGGGCCCCAGACACAGGGCTCTGGTGGCAGACTTTGAGGTTAT | 60 |
| Db | 2 | ATGGGAGACCCCAAGCTTGGGCCCCAGACACAGGGCTCTGGTGGCAGACTTTGAGGTTAT | 60 |
| QY | 61 | AAGCTAGGACAGAGGGTTATGTCCTGTGGAGCTGGCCCCGGGGAGGGCCACAGACTGAC | 120 |
| Db | 62 | AAGCTAGGACAGAGGGTTATGTCCTGTGGAGCTGGCCCCGGGGAGGGCCACAGACTGAC | 120 |
| QY | 121 | CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTGAGACCCGCTTCCGGCCGACCC | 180 |
| Db | 122 | CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTGAGACCCGCTTCCGGCCGACCC | 180 |
| QY | 181 | TTCTCTGATCTGCGGGCTCAGCTGCATGAGACCCCAAGGCTTCAGCCCAACGCTTCAACC | 240 |
| Db | 182 | TTCTCTGATCTGCGGGCTCAGCTGCATGAGACCCCAAGGCTTCAGCCCAACGCTTCAACC | 240 |

QY 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCCCACTGGGGCGCTTTGAGCCTTCTT 300
DB 242 CAGGCTCCGAGAACTTTTCAAGGGGGCCCCCACTGGGGCGCTTTGAGCCTTCTT 301
QY 301 CTCTTTGGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGAACAACAAGTGGGA 360
DB 302 GTCTTTGGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGAACAACAAGTGGGA 361
QY 361 CAAGTGCAGAGAGTGTGTGGCTTACCTGAGACGCGGCTGTGTGACTGTGATCCACAGC 420
DB 362 CAAGTGCAGAGAGTGTGTGGCTTACCTGAGACGCGGCTGTGTGACTGTGATCCACAGC 421
QY 421 AGTGGGGGCTGG 432
DB 422 AGTGGGGGCTGG 433

RESULT 10
US-10-311-455-201
; Sequence 201, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 201
; LENGTH: 6049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-201

Query Match 43.8%; Score 255.4; DB 15; Length 6049;
Best Local Similarity 74.4%; Pred. No. 1.6e-63;
Matches 322; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCAAGCTTGGGCCCCCAACACACGCGGCTGTGTGAGCACTTTGATGTTAT 60
DB 5001 ATGGCGATTTTATGTTGGGTTTATGATATACGGGTTTGTGTGATGATTTTATGATAT 5060
QY 61 AAGCTGAGGAGAGGGTTATGTCGTGAGACTGGCCCCGGGGAGGGGCCCGACGAGTAC 120
DB 5061 AAGCTGAGGAGAGGGTTATGTCGTGAGACTGGTTTGGGGAGGGTTTATGATGAT 5120
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGATGAGACCCCGCTTCGGCGCAC 180
DB 5121 TCGTGTATTAAGTATAGCGGGTATGAGATGATGAGATGAGATGAGATGAGATGAGAT 5180
QY 181 TTCTGTATCTGGGGCTCAGCTGATGATGACCCCAAGGCTCAGCCCAAGAGCTTCAAC 240
DB 5181 TTCTGTATCTGGGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGAT 5240
QY 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCCCACTGGGGCGCTTTGAGCCTTCTT 300
DB 5241 TAGGTTTTCGATGAACTTTTCAAGGGGGCCCCCACTGGGGCGCTTTGAGCCTTCTT 5300
QY 301 CTCTTTGGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGAACAACAAGTGGGA 360
DB 5301 GTTTTGGGGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5360

QY 361 CAAGTGCAGAGAGTGTGTGGCTTACCTGAGACGCGGCTGTGTGACTGTGATCCACAGC 420
DB 5361 TAAGTGTAGAGTGTGTGGCTTATTTTGAAGAGTGTGTGATGATGATGATGATGAT 5420
QY 421 AGTGGGGGCTGG 433
DB 5421 AGTGGGGGCTGG 5433

RESULT 11
US-10-311-455-202/c
; Sequence 202, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 202
; LENGTH: 6049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-202

Query Match 37.7%; Score 219.8; DB 15; Length 6049;
Best Local Similarity 70.0%; Pred. No. 2.9e-53;
Matches 296; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCAAGCTTGGGCCCCCAACACACGCGGCTGTGTGAGCACTTTGATGTTAT 60
DB 1049 ATAAAGACCCCAAGCTTGAACCCCAACACACGAACTTAATTAACAACTTTATTAAT 990
QY 61 AAGCTGAGGAGAGGGTTATGTCGTGAGACTGGCCCCGGGGAGGGGCCCGACGAGTAC 120
DB 989 AAGCTGAGGAGAGGGTTATGTCGTGAGACTGGCCCCGGGGAGGGGCCCGACGAGTAC 930
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGATGAGACCCCGCTTCGGCGCAC 180
DB 929 CCGCTGACCAAGCCATGAGCAACCAATTAATTAATTAATTAATTAATTAATTAAT 870
QY 181 TTCTGTATCTGGGGCTCAGCTGATGATGACCCCAAGGCTCAGCCCAAGAGCTTCAAC 240
DB 869 TTCTGTATCTGGGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGAT 810
QY 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCCCACTGGGGCGCTTTGAGCCTTCTT 300
DB 809 CAATATCCGATTAACCTTTTCAAAAAAACCAGCACTTAATTAATTAATTAATTAAT 750
QY 301 CTCTTTGGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGAACAACAAGTGGGA 360
DB 749 ATCTTTAAACTACATATATATTAATTAATTAATTAATTAATTAATTAATTAAT 690
QY 361 CAAGTGCAGAGAGTGTGTGGCTTACCTGAGACGCGGCTGTGTGACTGTGATCCACAGC 420
DB 689 CAATTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 630
QY 421 AGT 423
DB 629 AAT 627

RESULT 12

US-10-029-386-13384
Sequence 13384, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13384
LENGTH: 590
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR14.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
OTHER INFORMATION: SWISSPROT HIT: P70345, EVALU 2.00e-10
OTHER INFORMATION: NT HIT: g114751151, EVALU 0.00e+00
OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALU 1.00e-119
US-10-029-386-13384

Query Match

Best Local Similarity 26.1%; Score 152; DB 16; Length 590;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 GCGGAGTTTCACAGCTTATACGGGAGCGGGCCCTGGAGGAGCGGGCGCTGCGGGA 491
DB 25 GCGGAGTTTCACAGCTTATACGGGAGCGGGCCCTGGAGGAGCGGGCGCTGCGGGA 84
QY 492 GGGGAACCTGGCATCAGTGAGGACAGTGTCTGACGGGGCCGTGGCACTGGGGCCCTGGT 551
DB 85 GGGGAACCTGGCATCAGTGAGGACAGTGTCTGACGGGGCCGTGGCACTGGGGCCCTGGT 144
QY 552 AACTGTAGGGGCGCTTTTGTCTAGCAAGTGA 583
DB 145 AACTGTAGGGGCGCTTTTGTCTAGCAAGTGA 176

RESULT 13

US-10-029-386-27084
Sequence 27084, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 27084
LENGTH: 151
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR14.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALU 5.00e-70
OTHER INFORMATION: SWISSPROT HIT: P70345, EVALU 3.00e-11
OTHER INFORMATION: NT HIT: g114574571, EVALU 9.00e-80

US-10-029-386-27084

Query Match 25.9%; Score 151; DB 16; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 GCGGAGTTTCACAGCTTATACGGGAGCGGGCCCTGGAGGAGCGGGCGCTGCGGGA 491
DB 1 GCGGAGTTTCACAGCTTATACGGGAGCGGGCCCTGGAGGAGCGGGCGCTGCGGGA 60
QY 492 GGGGAACCTGGCATCAGTGAGGACAGTGTCTGACGGGGCCGTGGCACTGGGGCCCTGGT 551
DB 61 GGGGAACCTGGCATCAGTGAGGACAGTGTCTGACGGGGCCGTGGCACTGGGGCCCTGGT 120
QY 552 AACTGTAGGGGCGCTTTTGTCTAGCAAGTGA 582
DB 121 AACTGTAGGGGCGCTTTTGTCTAGCAAGTGA 151

RESULT 14

US-09-864-761-17690
Sequence 17690, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: AEOMICA-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 17690
LENGTH: 150

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL049829.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: NT HIT: D87461.1, EVALUATE 2.00e-79
OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUATE 8.00e-70
OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUATE 3.00e-11
US-09-864-761-17690

Query Match 25.7%; Score 150; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. No. 2.8e-33;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 433 GCGGAGTTCAAGCTCTATACGGGACCGGCGCTTGAGAGAGCGCGCTTGCGGAG 492
DB 1 GCGGAGTTCAAGCTCTATACGGGACCGGCGCTTGAGAGAGCGCGCTTGCGGAG 60
QY 493 GGGAACTGGGCGATGATGAGAGACAGTGTGACGGGGCGCTGGCACTGGGGCGCTGGTA 552
DB 61 GGGAACTGGGCGATGATGAGAGACAGTGTGACGGGGCGCTGGCACTGGGGCGCTGGTA 120
QY 553 ACTGTAGGGCGCTTTTGTCTAGCAAGTGA 582
DB 121 ACTGTAGGGCGCTTTTGTCTAGCAAGTGA 150

RESULT 15

US-10-402-017-9
Sequence 9, Application US/10402017
Publication No. US20030219871A1
GENERAL INFORMATION:
APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENBERGER
TITLE OF INVENTION: Host cells having improved survival properties and methods to get
FILE REFERENCE: Case 1/1314
CURRENT APPLICATION NUMBER: US/10/402,017
PRIOR FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: US 60/369,307
PRIOR APPLICATION NUMBER: April 2, 2002
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent version 3.1
SEQ ID NO 9
LENGTH: 660
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del16-83)
US-10-402-017-9

Query Match 24.9%; Score 145.2; DB 17; Length 660;
Best Local Similarity 58.2%; Pred. No. 7.7e-32;
Matches 255; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 95 GCCCGGGGAGAGGCCAGAGCTGACCGCTGACCAAGCATGCGGCGAGTGGAGATG 154
DB 185 GCCCGGGGAGAGGCCAGAGCTGACCGCTGACCAAGCATGCGGCGAGTGGAGATG 244
QY 155 AGTTGAG 214
DB 245 AGTTGAG 304
QY 215 CAGGCTCAGCCAG 274

DB 305 CAGGAGCTGATATCAAGCTTTGAACAGGTAGTGAATGAATCTTCCGGATGGGTAA 364
QY 275 ACTGGGCGCGCTTGTAGCTTCTTTCTTTGGGCGTGCACCTGTGTGAGAGTGTCA 334
DB 365 ACTGGGCGCGCTTGTAGCTTCTTTCTTTGGGCGTGCACCTGTGTGAGAGAGTGTCA 424
QY 335 ACAAGAGATGAACCACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 394
DB 425 ACAAGAGATGAACCACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484
QY 395 CGCGCTGTGCTGACTGATTCACAGAGTGGGGCTGGCGGAGTTGACAGCTTATACG 454
DB 485 ACCACTAGAGAGCTTGTGATCCAGAGACAGCGCGCTGGACACTTGTGGAACCTTACG 544
QY 455 GGGAGCGGCGCTGAG 514
DB 545 GAAACATGACAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 604
QY 515 CAGTGTGACGGGCGCG 532
DB 605 CAGTGTGACGGGCGCG 622

Search completed: April 10, 2005, 22:38:32
Job time : 502.358 secs

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Db 428 TTCTGTGATCTGGGGGCTCAGCTCATGTATGACCCCAAGCTCAGCCCAACACCTTCACC 369
Qy 241 CAGGTCTCCAGCAACATTTTTCAGAGGGGGCCCAACCTGGGGCCGCTTGTAGCTTCTT 300
Db 368 CAGGTCTCCAGCAACATTTTTCAGAGGGGGCCCAACCTGGGGCCGCTTGTAGCTTCTT 309
Qy 301 CTCTTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGTGGGA 360
Db 308 GTCTTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGTGGGA 249
Qy 361 CAAGTCAGAGATGTGATGTGGCCCTACCTGAGACCGGGCTGTGCTGATTCACACAGC 420
Db 248 CAAGTCAGAGATGTGATGTGGCCCTACCTGAGACCGGGCTGTGCTGATTCACACAGC 189
Qy 421 AGTGGGGGCTGGGGGCTGCAACAGCTCTTACGGGGAGCGGGCCCTGAGAGAGGGCGG 480
Db 188 AGTGGGGGCTGGGGGCTGCAACAGCTCTTACGGGGAGCGGGCCCTGAGAGAGGGCGG 129
Qy 481 CGTCTGCGAGAGGAGAACTGGGATCATGAGAGAGAGTGTGACGGGGGCGGTGGACATG 540
Db 128 CGTCTGCGAGAGGAGAACTGGGATCATGAGAGAGAGTGTGACGGGGGCGGTGGACATG 69
Qy 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 583
Db 68 GGGGCACTGGTAACTGTAGGGGCTTTTGTGCTAGCAAGTGA 26

RESULT 2
AY421020 582 bp DNA linear GSS 17-DEC-2003
LOCUS Homo sapiens BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence,
AY421020
VERSION AY421020.1 GI:39776977
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 582)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Interfing nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 582)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submision
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them
based on alignment.

FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/gene="BCL2L2"
/locus_tag="HCM7418"

ORIGIN

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Best Local Similarity 99.0%; Pred. No. 3.5e-132;
Matches 576; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 61 AAGCTGAGGCGAAGAGGTTATGTCTGTGAGCTGGCCCGGGAGGGCCAGACAGCTGAC 120
Qy 121 CCGCTGCACCAAGCCATGCGGGGAGCTGAGATGATGAGACCCGCTTCGGGCGGAC 180
Db 121 CCAGTGCACCAAGCCATGCGGGGAGCTGAGATGATGAGACCCGCTTCGGGCGGAC 180
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Db 241 CAGGTCTCCAGCAACTTTTTCAGAGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTT 300
Qy 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGTGGGA 360
Db 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGTGGGA 360
Qy 361 CAAGTCAGAGATGTGATGTGGCCCTACCTGAGACCGGGCTGTGCTGATTCACACAGC 420
Db 361 CAAGTCAGAGATGTGATGTGGCCCTACCTGAGACCGGGCTGTGCTGATTCACACAGC 420
Qy 421 AGTGGGGGCTGGGGGCTGCAACAGCTCTTACGGGGAGCGGGCCCTGAGAGAGGGCGG 480
Db 421 AGTGGGGGCTGGGGGCTGCAACAGCTCTTACGGGGAGCGGGCCCTGAGAGAGGGCGG 480
Qy 481 CGTCTGCGAGAGGAGAACTGGGATCATGAGAGAGAGTGTGACGGGGGCGGTGGACATG 540
Db 481 CGTCTGCGAGAGGAGAACTGGGATCATGAGAGAGAGTGTGACGGGGGCGGTGGACATG 540
Qy 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582
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RESULT 3
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LOCUS 56057367J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD617891
ACCESSION CD617891.1 GI:40266156
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 629)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK

COMMENT Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1..629

FEATURES
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| Qy | 61 | AAGCTGAGGCGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAAGGGCCAGCACTAC | 120 | | | | | | |
| Db | 547 | AAGCTGAGGCGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAAGGGCCAGCACTAC | 488 | | | | | | |
| Qy | 121 | CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGTGATTGAGACCCTTCCGGGCGAC | 180 | | | | | | |
| Db | 487 | CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGTGATTGAGACCCTTCCGGGCGAC | 428 | | | | | | |
| Qy | 181 | TTCTCTGATCTGGCGGCTCACTGTCATGTGACCCCAAGCTCACGCTTAC | 240 | | | | | | |
| Db | 427 | TTCTCTGATCTGGCGGCTCACTGTCATGTGACCCCAAGCTCACGCTTAC | 368 | | | | | | |
| Qy | 241 | CAGGCTCCGACGAACTTTTTCAAAGGGGCCCCCACTGGGGCCCTGTAGCTTCTT | 300 | | | | | | |
| Db | 367 | CAGGCTCCGACGAACTTTTTCAAAGGGGCCCCCACTGGGGCCCTGTGTAGCTTCTT | 308 | | | | | | |
| Qy | 301 | CTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGAGATGAACCACTGGTGGGA | 360 | | | | | | |
| Db | 307 | CTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGAGATGAACCACTGGTGGGA | 248 | | | | | | |
| Qy | 361 | CAAGTGACAGAGTGAATGTGTGGCTTACTGTGAGACGCGGCTGTGTGACTGATCCACAGC | 420 | | | | | | |
| Db | 247 | CAAGTGACAGAGTGAATGTGTGGCTTACTGTGAGACGCGGCTGTGTGACTGATCCACAGC | 188 | | | | | | |
| Qy | 421 | AGTGGGGGCTGGGCGGAGTTTCAACACTCTATTCGGGGAACGGGGCCCTTGAAGAGCGGG | 480 | | | | | | |
| Db | 187 | AGTGGGGGCTGGGCGGAGTTTCAACACTCTATTCGGGGAACGGGGCCCTTGAAGAGCGGG | 128 | | | | | | |
| Qy | 481 | CGTCTCGGGAAGGGGAACTGGGCACTCAGTGAAGAGACAGTGTGACGGGGCCGTGGCACTG | 540 | | | | | | |
| Db | 127 | CGTCTCGGGAAGGGGAACTGGGCACTCAGTGAAGAGACAGTGTGACGGGGCCGTGGCACTG | 68 | | | | | | |
| Qy | 541 | GGGGCCCTGTGTACTGTAGGGGCTTTTGTGTGACCAAGTGA | 583 | | | | | | |
| Db | 67 | GGGGCCCTGTGTACTGTAGGGGCTTTTGTGTGACCAAGTGA | 25 | | | | | | |
| RESULT 4 | | | | | | | | | |
| AL157542 | | 804 bp | mRNA | linear | EST 04-SEP-2003 | | | | |
| LOCUS | | | | | | | | | |
| DEFINITION | DKFZP761D0816.t1.761 (synonym: hamy2) Homo sapiens cDNA clone | | | | | | | | |
| ACCESSION | AL157542 | | | | | | | | |
| VERSION | AL157542.1 | GI:7057943 | | | | | | | |
| KEYWORDS | EST. | | | | | | | | |
| SOURCE | Homo sapiens (human) | | | | | | | | |
| ORGANISM | Homo sapiens | | | | | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | | | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | | | | | |
| TITLE | 1 (bases 1 to 804) | | | | | | | | |
| JOURNAL | Anorgew, W., Winkner, U., Mewes, W., Well, B. and Wiemann, S. | | | | | | | | |
| COMMENT | EST (Anorgew, W., Winkner, U., Mewes, H.W., Well, B. and Wiemann, S.) | | | | | | | | |
| | Unpublished (1999) | | | | | | | | |
| | Contact: MIPS | | | | | | | | |
| | MIPS | | | | | | | | |
| | Inpoteaedter Landstr.1, D-85764 Neuherberg, Germany | | | | | | | | |
| | This is the 5' sequence of the clone insert | | | | | | | | |
| | Clone from S. Wiemann, Molecular Genome Analysis, German Cancer | | | | | | | | |
| | Research Center (DKFZ); Email g.wiemann@dkfz-heidelberg.de; | | | | | | | | |
| | Sequenced by EMBL (European Molecular Biology Laboratories, | | | | | | | | |
| | Heidelberg/Germany) within the cDNA sequencing consortium of the | | | | | | | | |
| | German Genome Project. | | | | | | | | |
| | No sl sequence available. | | | | | | | | |
| | This clone (DKFZP761D0816) is available at the RZPD in Berlin. | | | | | | | | |
| | Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 | | | | | | | | |
| | Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. | | | | | | | | |
| | Location/Qualifiers | | | | | | | | |

| Query Match | Best Local Similarity | Matches | Score | DB | Length |
|----------------|--|------------|-------|--------|--------|
| 94.3% | 98.6% | 575 | 550 | 1 | 804 |
| Conservativity | 0 | Mismatches | 6 | Indels | 2 |
| Gap | 2 | Gap | 2 | Gap | 2 |
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| 134 | ATGGGACCCAGCCTCGGCCCCAGACACACAGGCGCTGTGTGGAGACTTTGTAGTAT | 193 | | | |
| 61 | AACTGAGGACGAAAGGTTATGTCTGTGGAGCTGGCCCCGGGGAGAGGCCACAGACGTAC | 120 | | | |
| 194 | AACTGAGGACGAAAGGTTATGTCTGTGGAGCTGGCCCCGGGGAGAGGCCACAGACGTAC | 253 | | | |
| 121 | CCGCTGCACCAAGGCGAGCGGGGAGCTGGGAGATAGATTCCAGACCCGCTTCCGGCGAC | 180 | | | |
| 254 | CCGCTGCACCAAGGCGAGCGGGGAGCTGGGAGATAGATTCCAGACCCGCTTCCGGCGAC | 313 | | | |
| 181 | TTCTCTGATCTGGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCACGACTTACAC | 240 | | | |
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| 241 | CAGGCTCCGACGAACTTTTCAAGGGGGCCCCAATGGGGCGCTTGTAGCTTCTTT | 300 | | | |
| 374 | CAGGCTCCGACGAACTTTTCAAGGGGGCCCCAATGGGGCGCTTGTAGCTTCTTT | 433 | | | |
| 301 | CTCTTTGGGCGCTGACCTGTGTGTGAGAGTGTCAACAAGAGATGAAACCACTGTGGGA | 360 | | | |
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| 361 | CAAGTGCAGAGTGGATGGTGGCCCTACCTGGAGACGGGCTGTGATGATCCACAGC | 420 | | | |
| 494 | CAAGTGCAGAGTGGATGGTGGCCCTACCTGGAGACGGGCTGTGATGATCCACAGC | 553 | | | |
| 421 | AGTGGGGCGTGGGCGGAGTTTCAACAGCTTATACGGGAGCGGGGCTTGGAGAGGCGCG | 480 | | | |
| 554 | AGTGGGGCGTGGGCGGAGTTTCAACAGCTTATACGGGAGCGGGGCTTGGAGAGGCGCG | 612 | | | |
| 481 | CGTCTCGCGGAGGGGAACTGGGCAATCAGTGAAGACAGTGTGACGGGGGCGGTGGCACTG | 540 | | | |
| 613 | CGTCTCGCGGAGGGGAACTGGGCAATCAGTGAAGACAGTGTGACGGGGGCGGTGGCACT | 671 | | | |
| 541 | GGGGCCCTGTGATCTGTAAGGGGCGCTTTTGTGCTGACCAAGTAA | 583 | | | |
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RESULT 5

BE793530

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

BE793530 1030 bp mRNA linear EST 20-SEP-2000

60159001F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5',

mRNA sequence.

BE793530

BE793530.1 GI:10214832

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 1030)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIML at: image.liml.gov
 Plate: LNC800 row: p column: 04
 High quality sequence start: 5
 High quality sequence stop: 709.
 Location/Qualifiers
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FEATURES

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 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match
 Best Local Similarity 94.1%; Score 548.4; DB 2; Length 1030;
 Matches 561; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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QY 1 ATGGCGACCCCGACCTCGGCCCGACACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60
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QY 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCGGGAGAGGGCCAGACAGCTGAC 120
DB 204 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCGGGAGAGGGCCAGACAGCTGAC 263
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DB 264 CCGCTCACCAACCCATGCGGGAGCTGAGATGATTCAGACCCCTTCCGGCGAC 323
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DB 564 AGTGGGGCTGGGGCGAGATTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGAGGGCGG 623
QY 481 CGTCTGGGGAGAGGGAATGGGCACTCAGTGAAGACAGTGTGAACGGGGCCGTTGACCTG 540
DB 624 CGTCTGGGGAGAGGGAATGGGCACTCAGTGAAGACAGTGTGAACGGGGCCGTTGACCTG 683
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Db

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 DEFINITION CN281020
 ACCESSION CN281020.1 GI:47297434
 VERSION EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Li, Y., Xu, C., Fang, R., Guebler, K., Rao, M. S., Mandalam, R.,
 Lebkowski, J. and Stanton, L. W.
 Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 Contact: Brandenberger R
 Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@genon.com
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FEATURES

Location/Qualifiers
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ORIGIN

Query Match
 Best Local Similarity 90.3%; Score 526.4; DB 7; Length 643;
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DB 168 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCGGGAGAGGGCCAGACAGCTGAC 227
QY 121 CCGCTGACCAACGACATGCGGGAGCTGAGATGATGAGACCGGCTTCGGGGCCAC 180
DB 228 CCGCTGACCAACGACATGCGGGAGCTGAGATGATGAGACCGGCTTCGGGGCCAC 287
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DB 348 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCCGCTTTGAGCTTTT 407
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QY 361 CAAGTGCAGAGATGATGTGGCTCACTGAGACCGGGCTGGTTCAGCTGATTCACAG 420

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| | | | |
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| Db | 528 | AGTGGGGGCTGGGCGGAGTTCAACGCTCTATACGGGGAACGGGCGCTTGGAGAGGCGCGG | 587 |
| Qy | 481 | CGTCTGCGGAGGGGAACCTGGGCATCATGTGAGGAGAACATGCTGACGGGGCCGTGGC | 536 |
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| DEFINITION | AY421022 | 582 bp | DNA |
| LOCUS | AY421022 | | linear |
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| ACCESSION | AY421022 | | |
| VERSION | AY421022.1 | | |
| KEYWORDS | GSS. | | |
| SOURCE | Mus musculus (house mouse) | | |
| ORGANISM | Mus musculus | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| REFERENCE | 1 (bases 1 to 582) | | |
| AUTHORS | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. | | |
| TITLE | Interfering nonneutral evolution from human-chimp-mouse orthologous gene trios | | |
| JOURNAL | Science 302 (5652), 1960-1963 (2003) | | |
| PUBMED | 14671302 | | |
| REFERENCE | 2 (bases 1 to 582) | | |
| AUTHORS | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA | | |
| COMMENT | This sequence as made by sequencing genomic exons and ordering them based on alignment. | | |
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| Qy | 61 | AAGCTGAGGACGAAGAGGTTATGCTGTGAGACTGGCCCCGGGAGAGGCCAGACCTGAC | 120 |
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| Db | 121 | CCGCTGACCAAGCCATGCGGGGAGCTGGAGACGAGTTTGAGACCCCGTTCCGGCGAC | 180 |
| Qy | 181 | TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCAAC | 240 |
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| Qy | 241 | CAGGCTTCGACGAATCTTTTCAGAGGGGGCCCAATCGGGGCGCGCTTGATGACCTTCTT | 300 |

[illegible]

JOURNAL
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
REFERENCE
6 (bases 1 to 1949)

| JOURNAL | MEDLINE | PUBMED | REFERENCE | AUTHORS |
|------------------------------------|---|--------------------|-----------|---------|
| JOURNAL 20530913 | Genome Res. | 10 (11), 1757-1771 | (2000) | |
| JOURNAL 11076861 | The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. | | | |
| JOURNAL Nature 409, | Functional annotation of a full-length mouse cDNA collection | | | |
| JOURNAL Nature 409, | 685-690 | (2001) | | |
| JOURNAL Nature 420, | The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. | | | |
| JOURNAL Nature 420, | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNA | | | |
| JOURNAL Nature 420, | 563-573 | (2002) | | |
| JOURNAL Nature 420, | 6 (bases 1 to 3487) | | | |
| JOURNAL Nature 420, | Adachi,J., Alizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukushima,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hirooka,T., Horii,F., Imotani,K., Ishii,Y., Itchi,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Komoh,M., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y. | | | |
| JOURNAL Submitted (10-JUN-2000) | Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-resgsc@riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216] | | | |
| TITLE | Please visit our web site (http://genome.gsc.riken.jp/) for further details. | | | |
| COMMENT | CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGGAGAAGCGCCGCACTGAGTTTATTTTTTTTNN 3'], cDNA was prepared by using triethanolamine-chloride reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence[5' GAAGAGAGAAGATCCAAGCATTCATTATTTAATAACCCCCCCC 3']. cDNA was cleaved with XhoI and SacI. Cloning sites, 5' end: SacI; 3' end: XhoI. Host: SOLR. | | | |
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| source | 1..3487 | | | |
| | /organism="Mus musculus" | | | |
| | /mol_type="mRNA" | | | |
| | /strain="C57BL/6J" | | | |
| | /db_xref="FANTOM_DB:1200009L24" | | | |
| | /db_xref="taxon:10090" | | | |
| | /clone="1200009L24" | | | |
| | /sex="male" | | | |
| | /tissue_type="lung" | | | |
| | /clone_lib="RIKEN full-length enriched mouse cDNA library" | | | |
| | /dev_stage="adult" | | | |
| | 209..790 | | | |
| | /note="unnamed protein product; Bcl2-like 2 | | | |
| | (MGD MG:108052) | | | |
| | putative" | | | |
| | /codon_start=1 | | | |
| | /protein_id="BAB23466.1" | | | |
| | /db_xref="GI:12836028" | | | |
| | /translation="MATPASTPTLVADTFVGYLRQGVYCGAPGPGPAAPDLHCAMRAAGDEFTRPRTPSDLAALOHFTGASAOORPTOVSDELFOGPMRGVLVAFFVGAACACBSVNKEMEPVGOVDWVAIVLETPLADMIHSSGGMAETPALYIGALEEARRLREGNAAVRITLVGAVALDALTVGAFFASK" | | | |
| | 3466..3471 | | | |

/note="putative"
 3487
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 polyA_site
 ORIGIN
 Query Match 89.7%; Score 522.8; DB 3; Length 3487;
 Bees Local Similarity 93.6%; Pred. No. 1.1e-119;
 Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

| Db | Accession | Version | Keywords | Source | Organism | Reference Authors |
|----|-----------|---|----------|--------|----------|-------------------|
| Db | 1 | ATGGGACCCAGAGCTCGGCCCCAGACACACAGGAGCTGTGTGAGAGACTTTGTAGATTAT | 60 | | | |
| Db | 209 | ATGGGACCCAGAGCTCAACCCAGACACAGGAGCTGTAGTGGCTGACTTTGTAGGGCTAT | 268 | | | |
| Db | 61 | AACTGAGGACGAAAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGGGGCCAGAGCTGAC | 120 | | | |
| Db | 269 | AAGCTGAGGACGAAAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGGGGCCAGAGCTGAC | 328 | | | |
| Db | 121 | CGGCTGACACCAAGGACATGCGGGGAGGCTGTGAGAGATAGTTTCGAGACCCGGCTTCGGGACAC | 180 | | | |
| Db | 329 | CCGCTGACACCAAGGACATGCGGGGAGGCTGTGAGAGATAGTTTCGAGACCCGGCTTCGGGACAC | 388 | | | |
| Db | 181 | TTCTCTGATCTGGGCGGCTCAGCTCATGTGACCCAGAGCTCAGCCAGACAGCTTCAAC | 240 | | | |
| Db | 389 | TTCTCTGATCTGGGCGGCTCAGCTCATGTGACCCAGAGCTCAGCCAGACAGCTTCAAC | 448 | | | |
| Db | 241 | CAGGCTCTCGACGAACTTTTTCAGAGGGGGCCCCAACTGGGGCGGCTTGTAGCTTCTTT | 300 | | | |
| Db | 449 | CAGGTTTCCGACGAACTTTTTCAGAGGGGGCCCCAACTGGGGCGGCTTGTAGCTTCTTT | 508 | | | |
| Db | 301 | CTCTTTGGGGGCTGACATGTGTGCTGAGAGTCAACAAAGAGATGGAACCACTGGTGGGA | 360 | | | |
| Db | 509 | GCTTTTGGGGGCTGACATGTGTGCTGAGAGTCAACAAAGAGATGGAACCTTTGGTGGGA | 568 | | | |
| Db | 361 | CAAGTGACAGAGTGAATGTGTGCTTACCTGAGAGAGCGGCTGTGCTGACTGATCAGAGC | 420 | | | |
| Db | 569 | CAAGTGACAGAGTGAATGTGTGCTTACCTGAGAGAGCGGCTGTGCTGACTGATCAGAGC | 628 | | | |
| Db | 421 | AGTGGGGGCTGGGCGGAGTTCAAGCTCTTATACGGGAGCGGGGCGCTGTGAGAGAGCGCGG | 480 | | | |
| Db | 629 | AGTGGGGGCTGGGCGGAGTTCAAGCTCTTATACGGGAGCGGGGCGCTGTGAGAGAGCGCGG | 688 | | | |
| Db | 481 | CGTCTGCGGGAGGGGAACTGGGCACTCACTGAGAGCACTGTGCTGAGCGGGGCGCTGTGAGAGC | 540 | | | |
| Db | 689 | CGTCTGCGGGAGGGGAACTGGGCACTCACTGAGAGCACTGTGCTGAGCGGGGCGCTGTGAGAGC | 748 | | | |
| Db | 541 | GGGGGCGCTGTGATCTGTAGGGGGCGCTTTTGTCTGAGCAAGTGA | 582 | | | |
| Db | 749 | GGGGGCGCTGTGATCTGTAGGGGGCGCTTTTGTCTGAGCAAGTGA | 790 | | | |

RESULT 10
 BY175200 969 bp mRNA linear EST 17-DEC-2002
 LOCUS BY175200 RIKEN full-length enriched, adult male testis Mus musculus
 DEFINITION CDNA clone 4930488D08 5', mRNA sequence.
 ACCESSION BY175200
 VERSION BY175200.1 GI:27128317
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 1 (bases 1 to 969)
 Okazaki, Y., Furuno, N., Kaasawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nishida, I., Otsu, M., Saito, R., Suzuki, H., Yamada, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schöndach, C., Gotohori, T., Balderelli, R., Hill, D. P., Bult, C.,
 Hume, D. A., Quackenbush, J., Schriml, L. M., Kanpin, A., Matsuda, H.,
 Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusic, V.,
 Chotha, C., Corbani, L. E., Cousins, S., Dalla, E., Dragan, T. A.,
 Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
 Gaidolidi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Guinacchi, M., Hirokawa, N., Jackson, J. J., Jarvis, E. D., Kanai, A.,

Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source
location/Qualifiers
1..662

/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone_id="FLP"
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ORIGIN

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Best Local Similarity 98.3%; Pred. No. 1.2e-118; Mismatches 534; Conservative 0; Indels 1; Gaps 1;

1 ATGGCGACCCAGCTGCGCCAGACACACGCGCTCTGTGGCAGACTTTAGTTAT 60
120 ATGGCGACCCAGCTGCGCCAGACACACGCGCTCTGTGGCAGACTTTAGTTAT 179
61 AAGCTGAGCAGAAAGGTTATGTCGTGAGCTGCGCCCGGGAGGGCCAGACTGAC 120
180 AAGCTGAGCAGAAAGGTTATGTCGTGAGCTGCGCCCGGGAGGGCCAGACTGAC 239
121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGATGTCGAGACCCGCTTCCGGCGAC 180
240 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGATGTCGAGACCCGCTTCCGGCGAC 299
181 TTCTCTGATGCGCGCTCAGCTGATGTAAGCCAGGCTCAGGCCAGCAAGCTTGACC 240
300 TTCTCTGATGCGCGCTCAGCTGATGTAAGCCAGGCTCAGGCCAGCAAGCTTGACC 359
241 CAGGCTCCGACGAATTTTCAAGGGGGCCCAACTGGGGCGCTTGAAGCTTCTTT 300
360 CAGGCTCCGACGAATTTTCAAGGGGGCCCAACTGGGGCGCTTGAAGCTTCTTT 419
301 CTCTTTGGGGCTGACCTGTGCTGAGAGTCAACAAGAGATGAAACCACTGTGGGA 360
420 GTCTTTGGGGCTGACCTGTGCTGAGAGTCAACAAGAGATGAAACCACTGTGGGA 479
361 CAAGTCAGAGAGTGA-TGGTGGCTTACTGAGACCGCGCTGTGACTGATCCACAG 419
480 CAAGTCAGAGAGTGA-TGGTGGCTTACTGAGACCGCGCTGTGACTGATCCACAG 539
420 CAGTGGGGGCTGGCGGAGTTCAAGCTCTAATACGGGACCGGGCCCTGAGAGAGCGG 479
540 CAGTGGGGGCTGGCGGAGTTCAAGCTCTAATACGGGACCGGGCCCTGAGAGAGCGG 599
480 GCGTCTCGGGAGGGGAATCTGGGATCACTGAGAGACAGTGTGACGGGGCCCTGAG 539
600 GCGTCTCGGGAGGGGAATCTGGGATCACTGAGAGACAGTGTGACGGGGCCCTGAG 659
540 GGG 542
660 GGG 662

RESULT 12
CD617890 627 bp mRNA linear EST 12-JAN-2004
LOCUS
DEFINITION 56057367H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD617890
VERSION CD617890.1 GI:40266155
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
EST.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source
location/Qualifiers
1..627

/organism="Homo sapiens"
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/clone_id="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

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Best Local Similarity 99.0%; Pred. No. 4.2e-114; Mismatches 503; Conservative 0; Indels 0; Gaps 0;

1 ATGGCGACCCAGCTGCGCCAGACACACGCGCTCTGTGGCAGACTTTAGTTAT 60
120 ATGGCGACCCAGCTGCGCCAGACACACGCGCTCTGTGGCAGACTTTAGTTAT 179
61 AAGCTGAGCAGAAAGGTTATGTCGTGAGCTGCGCCCGGGAGGGCCAGACTGAC 120
180 AAGCTGAGCAGAAAGGTTATGTCGTGAGCTGCGCCCGGGAGGGCCAGACTGAC 239
121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGATGTCGAGACCCGCTTCCGGCGAC 180
240 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGATGTCGAGACCCGCTTCCGGCGAC 299
181 TTCTCTGATGCGCGCTCAGCTGATGTAAGCCAGGCTCAGGCCAGCAAGCTTGACC 240
300 TTCTCTGATGCGCGCTCAGCTGATGTAAGCCAGGCTCAGGCCAGCAAGCTTGACC 359
241 CAGGCTCCGACGAATTTTCAAGGGGGCCCAACTGGGGCGCTTGAAGCTTCTTT 300
360 CAGGCTCCGACGAATTTTCAAGGGGGCCCAACTGGGGCGCTTGAAGCTTCTTT 419
301 CTCTTTGGGGCTGACCTGTGCTGAGAGTCAACAAGAGATGAAACCACTGTGGGA 360
420 GTCTTTGGGGCTGACCTGTGCTGAGAGTCAACAAGAGATGAAACCACTGTGGGA 479
361 CAAGTCAGAGAGTGA-TGGTGGCTTACTGAGACCGCGCTGTGACTGATCCACAGC 420
480 CAAGTCAGAGAGTGA-TGGTGGCTTACTGAGACCGCGCTGTGACTGATCCACAGC 539
420 AGTGGGGGCTGGCGGAGTTCAAGCTCTAATACGGGACCGGGCCCTGAGAGAGCGG 480
540 AGTGGGGGCTGGCGGAGTTCAAGCTCTAATACGGGACCGGGCCCTGAGAGAGCGG 599
481 CGTCTGCGGGAGGGGAATCTGGGATCAG 508
600 CGTCTGCGGGAGGGGAATCTGGGATCAG 627

RESULT 13
B1770566 697 bp mRNA linear EST 25-SEP-2001
LOCUS
DEFINITION 603060362F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5',
mRNA sequence.
ACCESSION B1770566
VERSION B1770566.1 GI:15762144
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
EST.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Straubeberg, Ph.D.

Email: c9abds-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM1526 row: k column: 15
 High quality sequence start: 21
 High quality sequence stop: 695.
 Location/Qualifiers
 1..697

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 /db_xref="taxon:9606"
 /clone="IMAGE:5209862"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_122"
 /note="Organ: pooled lung and spleen; Vector: pCMV-Sport6;
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
 anonymous pool of 24 week female lung, 16 week female
 spleen, and 20-22 week male spleen. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 026. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 82.9%; Score 483.4; DB 4; Length 697;
 Best Local Similarity 98.0%; Pred. No. 66-110;
 Matches 542; Conservative 0; Mismatches 6; Indels 5; Gaps 5;

1 ATGGGAGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAAGTTAT 60
 145 ATGGGAGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAAGTTAT 204
 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGCCAGAGCTGAC 120
 205 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGCCAGAGCTGAC 264
 121 CCGCTGCACCAAGCCATGCGGCGAGCTGAGATGATTGAGACCCGCTTCGGCGGAC 180
 265 CCGCTGCACCAAGCCATGCGGCGAGCTGAGATGATTGAGACCCGCTTCGGCGGAC 324
 181 TTCTCTGATCTGGGGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTCAAC 240
 325 TTCTCTGATCTGGGGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTCAAC 384
 241 CAGGCTCCGAGCAATTTTTCAGAGGGGGCCCAACTGCGGCTTGTGAGCTTCTTT 300
 385 CAGGCTCCGAGCAATTTTTCAGAGGGGGCCCAACTGCGGCTTGTGAGCTTCTTT 444
 301 CTCTTTGGGGGCTGACCTGTG-TGCTGAGAGTGTCAACAAGAGATGAAACCACTGATGG 359
 445 GTCTTTGGGGGCTGACCTGTG-TGCTGAGAGTGTCAACAAGAGATGAAACCACTGATGG 504
 360 ACAAGTGAAGAGTGAATGATGTGCTTACTT-GAGAGCGCGGCTGATGATGATCCACA 418
 505 ACAAGTGAAGAGTGAATGATGTGCTTACTT-GAGAGCGCGGCTGATGATGATCCACA 564
 419 GCAATGGGGGCTGAGCGGAGTTCAAGCTTATAC-GGGGACGGGGCCCTGAGAGAGCG 477
 565 GCAATGGGGGCTGAGCGGAGTTCAAGCTTATAC-GGGGACGGGGCCCTGAGAGAGCG 624
 478 CCGGCTCTGGGGGAGGGGGAAGCTGGGA-TCAATGAGAGAG-TGCTGACGGGGCCGCTGG 535
 625 CCGGCTCTGGGGGAGGGGGAAGCTGGGA-TCAATGAGAGAG-TGCTGACGGGGCCGCTGG 684
 536 CACTGGGGGGCCCT 548
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Db 685 CACTGGGGGGCCCT 697

RESULT 14
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 DEFINITION
 AGENCOURT_10030867 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6491566
 5', mRNA sequence.
 ACCESSION
 BUS03850
 VERSION
 BUS03850.1 GI:22810083
 EST
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 967)
 NIH-MGC <http://mgs.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT
 Contact: Robert Strausberg, Ph.D.
 Email: c9abds-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM14043 row: c column: 23
 High quality sequence stop: 524.
 Location/Qualifiers
 1..967

FEATURES

/organism="Mus musculus"
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 /db_xref="taxon:10090"
 /clone="IMAGE:6491566"
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 /lab_host="DH10B (phage-resistant)"
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 /note="Organ: eye; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 3.3 kb. Library enriched for
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 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 79.9%; Score 465.6; DB 5; Length 967;
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 Matches 544; Conservative 0; Mismatches 39; Indels 5; Gaps 5;

1 ATGGGAGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAAGTTAT 60
 130 ATGGGAGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAAGTTAT 189
 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGCCAGAGCTGAC 120
 190 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGCCAGAGCTGAC 249
 121 CCGCTGCACCAAGCCATGCGGCGAGCTGAGATGATTGAGACCCGCTTCGGCGGAC 180
 250 CCGCTGCACCAAGCCATGCGGCGAGCTGAGATGATTGAGACCCGCTTCGGCGGAC 309
 181 TTCTCTGATCTGGGGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTCAAC 240
 310 TTCTCTGATCTGGGGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTCAAC 369
 241 CAGGCTCCGAGCAATTTTTCAGAGGGGGCCCAACTGCGGCTTGTGAGCTTCTTT 300
 370 CAGGTTTCCAGCAATTTTTCAGAGGGGGCCCAACTGCGGCTTGTGAGCTTCTTT 429
 301 CTCTTTGGGGGCTGACCTGTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGATGG 360
 430 GTCTTTGGGGGCTGACCTGTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGATGG 489

QY 361 CAAGTCAGAGTAGTGTGGCCCTA-CCTGGAGACGGCGCTGTCAGATGATCCAG 419
 DB 490 CAAGTCAGAGTAGTGTGGCCCTA-CCTGGAGACGGCGCTGTCAGATGATCCAG 549
 QY 420 CAGT-GGGGGCTGGCGCGAGTTCAAGCTCTATACGGGAGC-GGGGCCCTGGAGAGCG 477
 DB 550 CAGTGGGGGGCTGGCGCGAGTTCAAGCTCTATACGGGAGC-GGGGCCCTGGAGAGCG 609
 QY 478 CGGGCTCTGGCGCGAGAGGGAACCTGGCATCACTGAGAGACAGTGTGAC-GGGGGCCGTGGC 536
 DB 610 CGGGCTCTGGCGCGAGAGGGAACCTGGCATCACTGAGAGACAGTGTGAC-GGGGGCCGTGGC 669
 QY 537 ACTGGGGGGCCCTGGATCTGT-AGGGGCTTTTGTGACGAGTGA 583
 DB 670 ACTGGGGGGCCCTGGATCTGTGAGGGGCTTTTGTGACGAGTGA 717
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 DEFINITION 17000532179318 GRN EB Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN281015
 VERSION CN281015.1 GI:47297429
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 516)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G., J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,
 Lebkowski, J. and Stanton, L. W.
 Transcriptional characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
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 FEATURES
 SOURCE
 1. 516
 Location/Qualifiers
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 /db_xref="taxon:9606"
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 derived from H1, H7 and H9 cells"
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 /note="Oligo dt primed, full-length enriched cDNA library
 from embryoid body outgrowths derived from hES cell lines
 H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
 conditions."
 ORIGIN
 Query Match 76.8%; Score 448; DB 7; Length 516;
 Best Local Similarity 98.9%; Pred. No. 4e-101;
 Matches 451; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ATGGCGACCCGAGCTGGCCCGCCAGACACACGGGCTCTGGTCAGACTTTGTAGTTAT 60
 DB 61 ATGGCGACCCGAGCTGGCCCGCCAGACACACGGGCTCTGGTCAGACTTTGTAGTTAT 120
 QY 61 AAGCTGAGGCGAGAGGGTTATGTCGTGAGAGCTGGCCCGGGGAGGGCCGACAGCTGAC 120
 DB 121 AAGCTGAGGCGAGAGGGTTATGTCGTGAGAGCTGGCCCGGGGAGGGCCGACAGCTGAC 180
 QY 121 CCGGTGACCAAGCCATGCGGGGAGCTGAGATGATGATTCAGAACCCGCTTCGGCGCAC 180
 DB 181 CCGGTGACCAAGCCATGCGGGGAGCTGAGATGATGATTCAGAACCCGCTTCGGCGCAC 240

QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCGAGGCTCAGGCCAGCAAGCTTCACC 240
 DB 241 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCGAGGCTCAGGCCAGCAAGCTTCACC 300
 QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGGGCCCAACTGGGGCCGCTTTAGCTTCCTT 300
 DB 301 CAGGTCTCCGATGAACCTTTTCAAGGGGGGCCCAACTGGGGCCGCTTTAGCTTCCTT 360
 QY 301 CTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAGAGATGAAACCACTGTGGGA 360
 DB 361 GTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAGAGATGAAACCACTGTGGGA 420
 QY 361 CAAGTCAGAGTAGTGTGGGCTTACCTGGAGACGGGGCTGTGCACTGGATCCAGAC 420
 DB 421 CAAGTCAGAGTAGTGTGGGCTTACCTGGAGACGGGGCTGTGCACTGGATCCAGAC 480
 QY 421 AGTGGGGCTGGCGGAGTTCAACAGCTCTATACGGG 456
 DB 481 AGTGGGGCTGGCGGAGTTCAACAGCTCTATACGGG 516

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 Job time : 2846.37 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2005, 22:21:58 ; Search time 19.5 Seconds

(without alignments)
738,834 Million cell updates/sec

Title: US-09-925-674B-7

Perfect score: 1007
Sequence: 1 MATPASPDRALVADPVG.....LTGAVLALVTVGAFPAASK 193Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Issued Patents AA:*
1: /cgn2_6/ptodate/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodate/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodate/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodate/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodate/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodate/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 1007 | 100.0 | 193 | 4 | US-09-155-327G-7 |
| 2 | 1007 | 100.0 | 193 | 4 | US-09-949-016-10928 |
| 3 | 1002 | 99.5 | 193 | 1 | US-08-798-897-4 |
| 4 | 1002 | 99.5 | 193 | 2 | US-08-798-897-4 |
| 5 | 1000 | 99.3 | 193 | 4 | US-08-155-327G-9 |
| 6 | 997 | 99.0 | 192 | 1 | US-08-798-897-6 |
| 7 | 997 | 99.0 | 192 | 2 | US-08-798-897-6 |
| 8 | 996 | 98.9 | 193 | 1 | US-08-798-897-3 |
| 9 | 996 | 98.9 | 193 | 2 | US-08-798-897-3 |
| 10 | 991 | 98.4 | 192 | 1 | US-08-798-897-5 |
| 11 | 991 | 98.4 | 192 | 2 | US-08-798-897-5 |
| 12 | 767 | 76.2 | 333 | 4 | US-09-155-327G-10 |
| 13 | 766 | 76.1 | 365 | 4 | US-09-149-476-696 |
| 14 | 766 | 76.1 | 365 | 4 | US-09-010-147B-24 |
| 15 | 433.5 | 43.0 | 411 | 4 | US-09-639-245-2 |
| 16 | 429.5 | 42.7 | 233 | 3 | US-08-333-565-59 |
| 17 | 428.5 | 42.6 | 233 | 1 | US-08-333-565-59 |
| 18 | 428.5 | 42.6 | 233 | 1 | US-08-081-448-6 |
| 19 | 428.5 | 42.6 | 233 | 1 | US-08-607-269-24 |
| 20 | 428.5 | 42.6 | 233 | 1 | US-08-471-058-14 |
| 21 | 428.5 | 42.6 | 233 | 2 | US-08-661-479-59 |
| 22 | 428.5 | 42.6 | 233 | 2 | US-08-470-670A-7 |
| 23 | 428.5 | 42.6 | 233 | 2 | US-08-471-057-14 |
| 24 | 428.5 | 42.6 | 233 | 3 | US-08-481-739-2 |
| 25 | 428.5 | 42.6 | 233 | 3 | US-09-167-921-2 |
| 26 | 428.5 | 42.6 | 233 | 3 | US-09-333-743-2 |
| 27 | 428.5 | 42.6 | 233 | 3 | US-08-461-511A-7 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 428.5 | 42.6 | 233 | 4 | US-08-470-865-14 | Sequence 14, Appl |
| 29 | 428.5 | 42.6 | 233 | 4 | US-09-155-327G-12 | Sequence 12, Appl |
| 30 | 428.5 | 42.6 | 233 | 5 | PCT-US94-07089-7 | Sequence 7, Appl |
| 31 | 428.5 | 42.6 | 233 | 5 | PCT-US95-04600-24 | Sequence 24, Appl |
| 32 | 425 | 42.2 | 225 | 3 | US-09-101-519-1 | Sequence 1, Appl |
| 33 | 423.5 | 42.1 | 233 | 1 | US-08-607-269-23 | Sequence 23, Appl |
| 34 | 423.5 | 42.1 | 233 | 5 | PCT-US95-04600-23 | Sequence 23, Appl |
| 35 | 413 | 41.0 | 236 | 1 | US-08-607-269-22 | Sequence 22, Appl |
| 36 | 413 | 41.0 | 236 | 3 | US-09-127-048-9 | Sequence 9, Appl |
| 37 | 413 | 41.0 | 236 | 5 | PCT-US95-04600-22 | Sequence 22, Appl |
| 38 | 412.5 | 41.0 | 239 | 1 | US-08-112-208C-10 | Sequence 10, Appl |
| 39 | 412.5 | 41.0 | 239 | 1 | US-08-248-819A-10 | Sequence 10, Appl |
| 40 | 412.5 | 41.0 | 239 | 2 | US-08-337-646A-10 | Sequence 10, Appl |
| 41 | 412.5 | 41.0 | 239 | 2 | US-08-856-531-10 | Sequence 10, Appl |
| 42 | 412.5 | 41.0 | 239 | 2 | US-08-856-531-10 | Sequence 10, Appl |
| 43 | 412.5 | 41.0 | 239 | 3 | US-09-127-048-8 | Sequence 8, Appl |
| 44 | 412.5 | 41.0 | 239 | 3 | US-08-927-326-10 | Sequence 10, Appl |
| 45 | 412.5 | 41.0 | 239 | 4 | US-09-379-820A-10 | Sequence 10, Appl |

ALIGNMENTS

```
RESULT 1
US-09-155-327G-7
Sequence 7, Application US/09155327G
Patent No. 6790637
GENERAL INFORMATION:
APPLICANT: AMRAD Operations Pty Ltd
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
FILE REFERENCE: 2096584
CURRENT APPLICATION NUMBER: US/09/155,327G
CURRENT FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PM8965
PRIOR FILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 193
TYPE: PRT
ORGANISM: HUMAN
US-09-155-327G-7

Query Match      100.0%; Score 1007; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MATPASPDRALVADPVGKLRKQGVCGAGPGEPPADPLHOAMRAAGDEFETRRRT 60
DB      1 MATPASPDRALVADPVGKLRKQGVCGAGPGEPPADPLHOAMRAAGDEFETRRRT 60
QY      61 FSDLAQLHTVPGSAQGRFTQVSDDELFOGGPNNGRLVAFVFGAALCAESVNMKEBPLVG 120
DB      61 FSDLAQLHTVPGSAQGRFTQVSDDELFOGGPNNGRLVAFVFGAALCAESVNMKEBPLVG 120
QY      121 QVGEWVAVYLETSLADMIHSSGMAEFTALYGGALBEARLRBGWMASTRVLTGVAL 180
DB      121 QVGEWVAVYLETSLADMIHSSGMAEFTALYGGALBEARLRBGWMASTRVLTGVAL 180
QY      181 GALVTGAFPAASK 193
DB      181 GALVTGAFPAASK 193

RESULT 2
US-09-949-016-10928
Sequence 10928, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10928
LENGTH: 193
TYPE: PRT
ORGANISM: Human
US-09-949-016-10928

Query Match 100.0%; Score 1007; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADVFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFEFRFRRT 60
DB 1 MATPASAPDTRALVADVFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFEFRFRRT 60
QY 61 FSDLAQLHTVTPGSAQQRFTQVSDLELFGGPNMGRVAFVFGALCAESVKNKEPVLVG 120
DB 61 FSDLAQLHTVTPGSAQQRFTQVSDLELFGGPNMGRVAFVFGALCAESVKNKEPVLVG 120
QY 121 QVQEMWVAYLETRLADWIIHSSGMAEFTLYGDGALBEARRLREGNMAVSRTVLTGAVAL 180
DB 121 QVQEMWVAYLETRLADWIIHSSGMAEFTLYGDGALBEARRLREGNMAVSRTVLTGAVAL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 3

US-08-798-897-4
Sequence 4, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483, 0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids

TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-798-897-4

Query Match 99.5%; Score 1002; DB 1; Length 193;
Best Local Similarity 99.5%; Pred. No. 1.2e-106;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADVFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFEFRFRRT 60
DB 1 MATPASAPDTRALVADVFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFEFRFRRT 60
QY 61 FSDLAQLHTVTPGSAQQRFTQVSDLELFGGPNMGRVAFVFGALCAESVKNKEPVLVG 120
DB 61 FSDLAQLHTVTPGSAQQRFTQVSDLELFGGPNMGRVAFVFGALCAESVKNKEPVLVG 120
QY 121 QVQEMWVAYLETRLADWIIHSSGMAEFTLYGDGALBEARRLREGNMAVSRTVLTGAVAL 180
DB 121 QVQEMWVAYLETRLADWIIHSSGMAEFTLYGDGALBEARRLREGNMAVSRTVLTGAVAL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 4

US-08-978-523-4
Sequence 4, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483, 0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-523-4

Query Match 99.5%; Score 1002; DB 2; Length 193;

Best Local Similarity 99.5%; Pred. No. 1.2e-106;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADYVGYKLRQGYVCGAGPGEPPADPLHQAAMRAAGDEFETRRRT 60
DB 1 MATPASAPDTRALVEDYVGYKLRQGYVCGAGPGEPPADPLHQAAMRAAGDEFETRRRT 60
QY 61 FSDLAQLHTVTPGSAOQRFQVSDDELFOGGMNGLVAFVFGAALCAESYNKEMEPLVG 120
DB 61 FSDLAQLHTVTPGSAOQRFQVSDDELFOGGMNGLVAFVFGAALCAESYNKEMEPLVG 120
QY 121 QVQEMWVAVLETRLADWTHSSGWAFFETALYGDALBEARLRGNMNAVTVLTGVAL 180
DB 121 QVQEMWVAVLETRLADWTHSSGWAFFETALYGDALBEARLRGNMNAVTVLTGVAL 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193

RESULT 5

US-09-155-327G-9
Sequence 9, Application US/09155327G
Patent No. 6790637
GENERAL INFORMATION:
APPLICANT: AMRAD Operations Pty Ltd
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
FILE REFERENCE: 2096584
CURRENT APPLICATION NUMBER: US/09/155,327G
CURRENT FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: P8965
PRIOR FILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 9
LENGTH: 193
TYPE: PRT
ORGANISM: Mouse
US-09-155-327G-9

Query Match 99.3%; Score 1000; DB 4; Length 193;
Best Local Similarity 99.0%; Pred. No. 2e-106;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADYVGYKLRQGYVCGAGPGEPPADPLHQAAMRAAGDEFETRRRT 60
DB 1 MATPASAPDTRALVADYVGYKLRQGYVCGAGPGEPPADPLHQAAMRAAGDEFETRRRT 60
QY 61 FSDLAQLHTVTPGSAOQRFQVSDDELFOGGMNGLVAFVFGAALCAESYNKEMEPLVG 120
DB 61 FSDLAQLHTVTPGSAOQRFQVSDDELFOGGMNGLVAFVFGAALCAESYNKEMEPLVG 120
QY 121 QVQEMWVAVLETRLADWTHSSGWAFFETALYGDALBEARLRGNMNAVTVLTGVAL 180
DB 121 QVQEMWVAVLETRLADWTHSSGWAFFETALYGDALBEARLRGNMNAVTVLTGVAL 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193

RESULT 6

US-08-798-897-6
Sequence 6, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guatella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-798-897-6

Query Match 99.0%; Score 997; DB 1; Length 192;
Best Local Similarity 99.5%; Pred. No. 4.3e-106;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATPASAPDTRALVADYVGYKLRQGYVCGAGPGEPPADPLHQAAMRAAGDEFETRRRT 61
DB 1 ATPASAPDTRALVEDYVGYKLRQGYVCGAGPGEPPADPLHQAAMRAAGDEFETRRRT 60
QY 62 SDLAQLHTVTPGSAOQRFQVSDDELFOGGMNGLVAFVFGAALCAESYNKEMEPLVG 121
DB 62 SDLAQLHTVTPGSAOQRFQVSDDELFOGGMNGLVAFVFGAALCAESYNKEMEPLVG 120
QY 122 QVQEMWVAVLETRLADWTHSSGWAFFETALYGDALBEARLRGNMNAVTVLTGVAL 181
DB 122 QVQEMWVAVLETRLADWTHSSGWAFFETALYGDALBEARLRGNMNAVTVLTGVAL 180
QY 182 ALVTGAFPAASK 193
DB 182 ALVTGAFPAASK 193

RESULT 7

US-08-978-523-6
Sequence 6, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guatella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-523-6

Query Match 99.0%; Score 997; DB 2; Length 192;
Best Local Similarity 99.5%; Pred. No. 4.3e-106;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATPASADTRALVADFGYKLRQKGYVCGAGGEGPADPLHQAMRAAGDEFETFRRT 61
DB 1 ATPASADTRALVADFGYKLRQKGYVCGAGGEGPADPLHQAMRAAGDEFETFRRT 60
QY 62 SDLAQLHVTTPGSAQGRFTQVSDLEFQGGPNMGRVAFVFGALCAESVNMKEPLVG 121
DB 61 SDLAQLHVTTPGSAQGRFTQVSDLEFQGGPNMGRVAFVFGALCAESVNMKEPLVG 120
QY 122 VOEMVAVIETRLADWIHSSGGMAEFTALYGDALAEARRLREGNMASVRTLGAVALG 181
DB 121 VOEMVAVIETRLADWIHSSGGMAEFTALYGDALAEARRLREGNMASVRTLGAVALG 180
QY 182 ALVTGAFPAK 193
DB 181 ALVTGAFPAK 192

RESULT 8

US-08-798-897-3
Sequence 3, Application US/08/798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-798-897-3

Query Match 98.9%; Score 996; DB 1; Length 193;
Best Local Similarity 98.4%; Pred. No. 5.7e-106;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASADTRALVADFGYKLRQKGYVCGAGGEGPADPLHQAMRAAGDEFETFRRT 60
DB 1 MATPASADTRALVADFGYKLRQKGYVCGAGGEGPADPLHQAMRAAGDEFETFRRT 60
QY 61 FSDLAQLHVTTPGSAQGRFTQVSDLEFQGGPNMGRVAFVFGALCAESVNMKEPLVG 120
DB 61 FSDLAQLHVTTPGSAQGRFTQVSDLEFQGGPNMGRVAFVFGALCAESVNMKEPLVG 120
QY 121 VOEMVAVIETRLADWIHSSGGMAEFTALYGDALAEARRLREGNMASVRTLGAVAL 180
DB 121 VOEMVAVIETRLADWIHSSGGMAEFTALYGDALAEARRLREGNMASVRTLGAVAL 180
QY 181 GALVTGAFPAK 193
DB 181 GALVTGAFPAK 193

RESULT 9

US-08-978-523-3
Sequence 3, Application US/08/78523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid

STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-523-3

Query Match 98.4%; Score 996; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 5,76-106;
Matches 199; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGPGEPAADPLHQAAMRAAGDEFETRFRRTF 60
DB 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGPGEPAADPLHQAAMRAAGDEFETRFRRTF 60
QY 61 PSDLAAGLHTVTPGSAOQRFQVSDDELFOGSPNMGRLVAFVFGAALCAESYNKMEPLVQ 120
DB 61 PSDLAAGLHTVTPGSAOQRFQVSDDELFOGSPNMGRLVAFVFGAALCAESYNKMEPLVQ 120
QY 121 VOEWNVAVYLETBLADWTHSSGNAEFTALYGDGALBEARLRGNMNAVTVTLTGAVALG 180
DB 121 VOEWNVAVYLETBLADWTHSSGNAEFTALYGDGALBEARLRGNMNAVTVTLTGAVALG 180
QY 181 GALTVGAFPAK 193
DB 181 GALTVGAFPAK 193

RESULT 10
US-08-798-897-5
Sequence 5, Application US/08798897
Patent No. 5789201

GENERAL INFORMATION:

APPLICANT: Guastella, John

TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2

TITLE OF INVENTION: Homologue

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESSES:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/798, 897

FILING DATE: February 11, 1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Emond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-798-897-5

Query Match 98.4%; Score 991; DB 1; Length 192;
Best Local Similarity 98.4%; Pred. No. 2,1e-105;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASAPDTRALVADPVGYKLRQKGYVCGAGPGEPAADPLHQAAMRAAGDEFETRFRRTF 61
DB 2 ATPASAPDTRALVADPVGYKLRQKGYVCGAGPGEPAADPLHQAAMRAAGDEFETRFRRTF 61

DB 1 ATPASAPDTRALVADPVGYKLRQKGYVCGAGPGEPAADPLHQAAMRAAGDEFETRFRRTF 60
QY 62 SDLAAGLHTVTPGSAOQRFQVSDDELFOGSPNMGRLVAFVFGAALCAESYNKMEPLVQ 121
DB 62 SDLAAGLHTVTPGSAOQRFQVSDDELFOGSPNMGRLVAFVFGAALCAESYNKMEPLVQ 120

QY 122 VOEWNVAVYLETBLADWTHSSGNAEFTALYGDGALBEARLRGNMNAVTVTLTGAVALG 181
DB 122 VOEWNVAVYLETBLADWTHSSGNAEFTALYGDGALBEARLRGNMNAVTVTLTGAVALG 180

QY 182 ALTVGAFPAK 193
DB 181 ALTVGAFPAK 192

RESULT 11
US-08-978-523-5
Sequence 5, Application US/08978523
Patent No. 5883229

GENERAL INFORMATION:

APPLICANT: Guastella, John

TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2

TITLE OF INVENTION: Homologue

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESSES:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978, 523

FILING DATE: herewith

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Emond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-978-523-5

Query Match 98.4%; Score 991; DB 2; Length 192;
Best Local Similarity 98.4%; Pred. No. 2,1e-105;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASAPDTRALVADPVGYKLRQKGYVCGAGPGEPAADPLHQAAMRAAGDEFETRFRRTF 61
DB 2 ATPASAPDTRALVADPVGYKLRQKGYVCGAGPGEPAADPLHQAAMRAAGDEFETRFRRTF 60

QY 62 SDLAAGLHTVTPGSAOQRFQVSDDELFOGSPNMGRLVAFVFGAALCAESYNKMEPLVQ 121
DB 62 SDLAAGLHTVTPGSAOQRFQVSDDELFOGSPNMGRLVAFVFGAALCAESYNKMEPLVQ 120

QY 122 VOEWNVAVYLETBLADWTHSSGNAEFTALYGDGALBEARLRGNMNAVTVTLTGAVALG 181
DB 122 VOEWNVAVYLETBLADWTHSSGNAEFTALYGDGALBEARLRGNMNAVTVTLTGAVALG 180

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Db      121 VQDMVTYLETRLADWTHSSGGWAEFTALYGDALAEARLHSGMNASRTVLTGAVALG 180
QY      182 ALVTGAFPAK 193
Db      181 ALVTGAFPAK 192

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RESULT 12

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US-09-155-327G-10
Sequence 10, Application US/09155327G
Patent No. 6790637
GENERAL INFORMATION:
APPLICANT: AMRAD Operations Pty Ltd
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
FILE REFERENCE: 2096584
CURRENT APPLICATION NUMBER: US/09/155,327G
CURRENT FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PN8965
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 333
TYPE: PRT
ORGANISM: murine
US-09-155-327G-10

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Query Match      76.2%; Score 767; DB 4; Length 333;
Best Local Similarity 74.4%; Pred. No. 2,2e-79;
Matches 157; Conservative 6; Mismatches 18; Indels 30; Gaps 4;

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QY      1 MATPASAPTRALVADFYGYKLRQKGYCGAGSGRSPADPLHQMRAAGDEFETFRFRT 60
Db      1 MATPASAPTRALVADFYGYKLRQKGYCGAGSGRSPADPLHQMRAAGDEFETFRFRT 60
QY      61 FSDLAQLHVTGSAQGRFTQVSDLFQGGPWNGLVAFVFGALCAESYKKEWEPVYG 120
Db      61 FSDLAQLHVTGSAQGRFTQVSDLFQGGPWNGLVAFVFGALCAESYKKEWEPVYG 120
QY      121 QVOEMVAVYLETRLADWTHSSGGWAEFTALYGDALAEARLHSGMNASRTVLTGAVALG 164
Db      121 QVOEMVAVYLETRLADWTHSSGGWAEFTALYGDALAEARLHSGMNASRTVLTGAVALG 164
QY      165 -GN-----WASVFTVLTGAVALGA 182
Db      180 PGNAGPVIMSLERKKEADARSLYGVGVYGA 210

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RESULT 13

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US-09-149-476-696
Sequence 696, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336

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EARLIER APPLICATION NUMBER: 60/040,163
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EARLIER APPLICATION NUMBER: 60/047,600
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EARLIER APPLICATION NUMBER: 60/047,615
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EARLIER APPLICATION NUMBER: 60/047,613
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06

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EARLIER APPLICATION NUMBER: 60/056, 886
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048, 964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057, 650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/057, 669
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057, 669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049, 610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061, 060
EARLIER FILING DATE: 1997-10-02

Query Match 76.1%; Score 766; DB 4; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.3e-79;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGKRLAKQGYVCGAGGEGRAADPLQNMMAADDEPTERRRT 60
DB 1 MATPASAPDTRALVADPVGKRLAKQGYVCGAGGEGRAADPLQNMMAADDEPTERRRT 60
QY 61 FSDLAQLHTPGSAOORFTQVSDDELFOGAPNMGRVAFVFGAALCAESVNMKEPVLG 120
DB 61 FSDLAQLHTPGSAOORFTQVSDDELFOGAPNMGRVAFVFGAALCAESVNMKEPVLG 120
QY 121 QVQEMWVAVLETRLADWIHSSGGM 144
DB 121 QVQEMWVAVLETRLADWIHSSGGM 144

RESULT 14
US-09-010-147B-24
Sequence 24, Application US/09010147B
Patent No. 6653445
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: Human Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,147B
FILING DATE: 12-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-Jan-1997
APPLICATION NUMBER: US 60/034,204
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: P353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-010-147B-24

Query Match 76.1%; Score 766; DB 4; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.3e-79;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASADPTRALVADFYGYKLRQGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASADPTRALVADFYGYKLRQGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHTVTPGSAQQRFTQVSDLPFGGPNWGRVAFVFGALCAESVYKMEPLVG 120
DB 61 FSDLAQLHTVTPGSAQQRFTQVSDLPFGGPNWGRVAFVFGALCAESVYKMEPLVG 120
QY 121 QVQEMMVAVLETPLADWTHSSGGW 144
DB 121 QVQEMMVAVLETPLADWTHSSGGW 144

RESULT 15
US-09-639-245-2
Sequence 2, Application US/09639245
Patent No. 6737511
GENERAL INFORMATION:
APPLICANT: Youle et al.
TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL
TITLE OF INVENTION: FUSION PROTEIN INHIBITS APOPTOSIS
FILE REFERENCE: 4239-55417
CURRENT APPLICATION NUMBER: US/09/639,245
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/149,220
PRIOR FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: genetic fusion
US-09-639-245-2

Query Match 43.0%; Score 433.5; DB 4; Length 411;
Best Local Similarity 39.9%; Pred. No. 5.2e-41;
Matches 93; Conservative 26; Mismatches 63; Indels 51; Gaps 4;

QY 11 RALVADFYGYKLRQGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 39
DB 26 RELVADFYGYKLRQGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 85
QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAQLHTVTPGSAQQRFTQ 81

DB 86 NGATTAHSSLDAREVTPMAAVVQALREAGDEFELRRTAFSDLTSLHTTGTAYQSFEQ 145
QY 82 VSDLEFQGGPNWGRVAFVFGALCAESVYKMEPLVQVQVQEMMVAVLETPLADWTHSS 141
DB 146 VVVELFRDGVNWRIVAFVFGALCAESVYKMEPLVQVQVQEMMVAVLETPLADWTHSS 205
QY 142 GGAEEFTALYDGLAEARLRRE--GNMASVRTLGAVALGALVTGAFPFAS 192
DB 206 GGMDTVELYGNMAAESRKGQERFNRWFLTGVTAGVVLSSLPFRKAYSA 258

Search completed: April 10, 2005, 22:45:27
Job time : 21.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2005, 20:17:32 ; Search time 59 Seconds
(without alignments)
1675.106 Million cell updates/sec

Title: US-09-925-674B-7
Perfect score: 1007
Sequence: 1 MATPASAPDTRALVADPVG.....LTGAVLALGALVTGAFPPASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1007 | 100.0 | 193 | 1 | BCLW_HUMAN |
| 2 | 1000 | 99.3 | 193 | 1 | BCLW_MOUSE |
| 3 | 996 | 98.9 | 193 | 2 | O88956 |
| 4 | 996 | 98.9 | 219 | 2 | Q7TS60 |
| 5 | 987 | 98.0 | 192 | 2 | Q6A093 |
| 6 | 951 | 94.4 | 193 | 2 | O8CGI4 |
| 7 | 761 | 75.6 | 178 | 2 | O8CFR2 |
| 8 | 761 | 75.6 | 178 | 2 | O9CWM5 |
| 9 | 651.5 | 64.7 | 188 | 2 | O6GP82 |
| 10 | 646.5 | 64.2 | 228 | 1 | ARI_XENLA |
| 11 | 440.5 | 43.0 | 233 | 2 | O9MYW4 |
| 12 | 433.5 | 43.7 | 233 | 2 | O8SQ42 |
| 13 | 432.5 | 42.9 | 229 | 1 | BCLX_CHICK |
| 14 | 431.5 | 42.9 | 233 | 1 | BCLX_PIG |
| 15 | 431.5 | 42.9 | 233 | 2 | O9N1A2 |
| 16 | 428.5 | 42.6 | 233 | 1 | BCLX_HUMAN |
| 17 | 428.5 | 42.6 | 233 | 1 | BCLX_MOUSE |
| 18 | 428.5 | 42.6 | 233 | 1 | BCLX_MOUSE |
| 19 | 428.5 | 42.6 | 233 | 1 | BCLX_MOUSE |
| 20 | 428.5 | 42.6 | 233 | 2 | O9MZS7 |
| 21 | 423.5 | 42.1 | 233 | 1 | BCL2_CHICK |
| 22 | 416.5 | 41.4 | 229 | 1 | BCL2_BOVIN |
| 23 | 414 | 41.1 | 236 | 1 | BCL2_RAT |
| 24 | 413 | 41.0 | 236 | 1 | BCL2_MOUSE |
| 25 | 413 | 41.0 | 236 | 2 | O7TSN8 |
| 26 | 413 | 41.0 | 239 | 1 | BCL2_HUMAN |
| 27 | 412.5 | 41.0 | 239 | 1 | BCL2_HUMAN |
| 28 | 403 | 40.0 | 236 | 1 | BCL2_CRITLO |
| 29 | 402.5 | 40.0 | 239 | 2 | O90ZS8 |
| 30 | 402.5 | 40.0 | 239 | 2 | O7SSV7 |
| 31 | 402 | 39.9 | 79 | 2 | Q7TS61 |

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| 32 | 401 | 39.8 | 180 | 2 | Q9BDD5 | Q9bdd5 bos taurus |
| 33 | 401 | 39.8 | 217 | 2 | O9N3S5 | O9n3s5 mus musculus |
| 34 | 399 | 39.6 | 236 | 2 | O923R6 | O923r6 cricetus |
| 35 | 398.5 | 39.6 | 180 | 2 | O9BDX7 | O9bdx7 bos taurus |
| 36 | 398.5 | 39.6 | 201 | 2 | O6GUL5 | O6gul5 xenopus tro |
| 37 | 396.5 | 39.4 | 235 | 2 | O8I008 | O8i008 felle silve |
| 38 | 396 | 39.3 | 236 | 2 | O6R755 | O6r755 canis faml |
| 39 | 380.5 | 37.8 | 284 | 2 | O7TS62 | O7ts62 ratus norv |
| 40 | 374.5 | 37.2 | 188 | 2 | O9CWX2 | O9cwx2 mus musculu |
| 41 | 374.5 | 37.2 | 225 | 2 | O35843 | O35843 mus musculu |
| 42 | 373.5 | 37.1 | 188 | 2 | O9H1R6 | O9h1r6 homo sapien |
| 43 | 373 | 37.0 | 204 | 2 | O90ZH2 | O90zh2 xenopus lae |
| 44 | 371 | 36.8 | 204 | 1 | ARI_XENLA | O91828 xenopus lae |
| 45 | 366.5 | 36.4 | 153 | 2 | Q7YB6 | Q7yrb6 canis faml |

ALIGNMENTS

RESULT 1
BCLW_HUMAN STANDARD; PRT; 193 AA.
ID BCLW_HUMAN
AC Q92843;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Apoptosis regulator Bcl-w (Bcl-2-like 2 protein).
GN Name=BCL2L2; Synonyms=BCLW, KIAA0271;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.",
RL Oncogene 13:665-675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ichikawa K.-I., Ohira M., Kawarabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.",
RL DNA Res. 3:321-329(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=92388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Khatami M.R., Lander E.S., Linton J.M., Rozen S., White O., Holt A.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.L., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Spatlenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Botterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- FUNCTION: Promotes cell survival.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
 CC in a wide range of tissues, with highest levels in brain, colon,
 CC and salivary gland.
 CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
 CC function.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -----
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 CC -----
 CC DR EMBL, U59747; AAB09055.1; -
 CC DR EMBL, D87461; BAA19666.2; ALT_INIT.
 CC DR EMBL, BC021198; AAH21198.1; -
 CC DR PDB; 1MK3; NMR; A=2-172.
 CC DR PDB; 1OOL; NMR; A=1-183.
 CC DR GeneW; HGNC:995; BCL2L2.
 CC DR H-INDB; HIX0011536; -
 CC DR MIM; 601931; -
 CC DR GO; GO:0005737; C:cytoplasm; NAS.
 CC DR GO; GO:0006916; P:anti-apoptosis; TAS.
 CC DR GO; GO:0007283; P:apoptosis; TAS.
 CC DR InterPro; IPR000712; Bcl2_BH.
 CC DR InterPro; IPR003093; Bcl2_BH.
 CC DR InterPro; IPR002475; Bcl2_family.
 CC DR Pfam; PF00452; Bcl-2; 1.
 CC DR Pfam; PF02180; BH4; 1.
 CC DR PROSITE; PS50062; BCL2_FAMILY; 1.
 CC DR PROSITE; PS01080; BH1; 1.
 CC DR PROSITE; PS01258; BH2; 1.
 CC DR PROSITE; PS01260; BH4_1; 1.
 CC DR PROSITE; PS50063; BH4_2; 1.
 CC DR 3D-structure; Apoptosis.
 CC KW DOMAIN 9 29 BH4.
 CC FT DOMAIN 85 104 BH1.
 CC FT DOMAIN 136 151 BH2.
 CC FT SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;
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 CC Best Local Similarity 100.0%; Pred. NO. 4.3e-62;
 CC Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 CC Db 1 MATPASPAPDTRALVADFGVYLRQKGYVCGAGPGEPAADPLHQAQRAAGDEFEFRRT 60
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 CC Db 61 FSDLAALQHTWPGSAQGRFTQVSELTQGGGPNMGRALVAFVFGAALCAESVNMKEPLVG 120
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 CC Db 121 QVQEMWVAIYETRLADWTHSSGGWAEFTALYGDALAEARLRLEGGNASTRTLTGAVL 180
 CC QY 121 QVQEMWVAIYETRLADWTHSSGGWAEFTALYGDALAEARLRLEGGNASTRTLTGAVL 180
 CC Db 121 QVQEMWVAIYETRLADWTHSSGGWAEFTALYGDALAEARLRLEGGNASTRTLTGAVL 180
 CC QY 181 GALVTGAFPAK 193
 CC Db 181 GALVTGAFPAK 193
 CC
 CC RESULT 2
 CC BCLW_MOUSE STANDARD; PRT; 193 AA.
 CC ID BCLW_MOUSE
 CC AC P70345;
 CC DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Apoptosis regulator Bcl-2 (Bcl-2-like 2 protein).
 GN Name=Bcl2l2; Synonyms=Bclw;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358615; PubMed=8761287;
 RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,
 RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,
 RT "bcl-w", a novel member of the bcl-2 family, promotes cell survival.";
 RL Oncogene 13:665-675 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98160183; PubMed=9500547;
 RA Roes A.J., Mayre K.G., Moss J.E., Parlow A.F., Skinner M.K.,
 RA Russell L.D., Macgregor G.R.;
 RT "Testicular degeneration in Bclw-deficient mice.";
 RL Nat. Genet. 18:251-256 (1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotojori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chotila C., Cobari L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazier K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kanagaya A., Kurochik I.V., Lee Y., Lemhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszewski B., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 CC -1- FUNCTION: Promotes cell survival.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
 CC in a wide range of tissues, with highest levels in brain, colon,
 CC and salivary gland.
 CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
 CC function.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -----
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CC -----

DR EMBL; U59746; AAB09056.1; -

DR EMBL; AF030769; AAB86430.1; -

DR EMBL; AF015644; BAB29912.1; -

DR HSSP; Q92843; 100L.

DR MGD; MGI:108052; Bcl2l2.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0006915; P:apoptosis; IDA.

DR InterPro; IPR000712; Bcl2_BH.

DR InterPro; IPR003093; Bcl2_BH4.

DR InterPro; IPR002475; Bcl2_family.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR PROSITE; PS50062; BCL2_FAMILY; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.

DR PROSITE; PS01260; BH4_1; 1.

DR PROSITE; PS50063; BH4_2; 1.

KM Apoptosis.

FT DOMAIN 9 29 BH4.

FT DOMAIN 85 104 BH1.

FT DOMAIN 136 151 BH2.

SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;

Query Match 99.3%; Score 1000; DB 1; Length 193;
Best Local Similarity 99.0%; Pred. No. 1,86-81;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPPASAPDTRALVADPVGKYLROKGYVCGAGPGEAPADPLQAMRAAGDEFTRRRT 60
DB 1 MATPASFPDTRALVADPVGKYLROKGYVCGAGPGEAPADPLQAMRAAGDEFTRRRT 60

QY 61 FSDLAQLHTVTPGSAOQRFQVSDDELFGGPNNGRLVAFVFGALCAESVNMKEPLVG 120
DB 61 FSDLAQLHTVTPGSAOQRFQVSDDELFGGPNNGRLVAFVFGALCAESVNMKEPLVG 120

QY 121 QVDEMMVAVLETRLDWIHSSGGWAEFTALYGDALBEARLRGNMNASVRYTLTGAVAL 180
DB 121 QVDEMMVAVLETRLDWIHSSGGWAEFTALYGDALBEARLRGNMNASVRYTLTGAVAL 180

QY 181 GALVTGAFPAK 193
DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193
DB 181 GALVTGAFPAK 193

RESULT 3
088996 PRELIMINARY; PRT; 193 AA.

AC 088996;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Bcl-w (Hypothetical protein).
GN Name=bcl-w;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RC MEDLINE=99292146; PubMed=10366024; DOI=10.1016/S0306-4522(98)00642-3;
RA Hamner S., Skoglosa Y., Lindholm D.;
RT "Differential expression of bcl-w and bcl-x messenger RNA in the
RT developing and adult rat nervous system.";
RL Neuroscience 91:673-684(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RC MEDLINE=22672518; PubMed=12787069;
RA Itoh T., Itoh A., Pleasure D.;

RT "Bcl-2-related protein family gene expression during oligodendroglial
RT differentiation.";
RL J. Neurochem. 85:1500-1512(2003).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feltingold E.A., Grouse L.H., Derje J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hale F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udell T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalley D.E., Scherch J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Straubeberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096291; AAC64200.1; -
DR EMBL; AY185098; AAC64468.1; -
DR EMBL; BC074021; AAH74021.1; -
DR HSSP; Q92843; 100L.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
KM Hypothetical protein.
SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;

Query Match 98.4%; Score 996; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 4,1e-81;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAPPASAPDTRALVADPVGKYLROKGYVCGAGPGEAPADPLQAMRAAGDEFTRRRT 60
DB 1 MATPASFPDTRALVADPVGKYLROKGYVCGAGPGEAPADPLQAMRAAGDEFTRRRT 60

QY 61 FSDLAQLHTVTPGSAOQRFQVSDDELFGGPNNGRLVAFVFGALCAESVNMKEPLVG 120
DB 61 FSDLAQLHTVTPGSAOQRFQVSDDELFGGPNNGRLVAFVFGALCAESVNMKEPLVG 120

QY 121 QVDEMMVAVLETRLDWIHSSGGWAEFTALYGDALBEARLRGNMNASVRYTLTGAVAL 180
DB 121 QVDEMMVAVLETRLDWIHSSGGWAEFTALYGDALBEARLRGNMNASVRYTLTGAVAL 180

QY 181 GALVTGAFPAK 193
DB 181 GALVTGAFPAK 193

RESULT 4

| ID | Q77S60 | PRELIMINARY; | PRT; | 219 AA. |
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| AC | Q77S60; | | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Created) | | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) | | | |
| DT | 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) | | | |
| OS | BCL-WBL. | | | |
| OS | Rattus norvegicus (Rat). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | | |
| RN | NCBI_TaxID=10116; | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | SPRAIN=Sprague-Dawley; | | | |
| RX | MEDLINE=22672518; PubMed=12787069; | | | |
| RA | Itoh T., Itoh A., Pleasure D.; | | | |
| RT | "Bcl-2-related protein family gene expression during oligodendroglial | | | |
| RT | differentiation."; | | | |
| RL | J. Neurochem. 85:1500-1512 (2003). | | | |
| DR | EMBL: AY185100; AA064470.1; -- | | | |
| DR | HSSP: Q07817; 1R2D. | | | |
| DR | GO: 0042381; P:regulation of apoptosis; IEA. | | | |
| DR | InterPro: IPR007012; Bcl2_BH. | | | |
| DR | InterPro: IPR003093; Bcl2_BH4. | | | |
| DR | InterPro: IPR002475; BCL2_family. | | | |
| DR | Pfam: PF00452; Bcl1-2; 1. | | | |
| DR | Pfam: PF02180; BH4; 1. | | | |
| DR | SMART: SM00337; BCL; 1. | | | |
| DR | SMART: SM00265; BH4; 1. | | | |
| DR | PROSITE: PS50062; BCL2_FAMILY; 1. | | | |
| DR | PROSITE: PS01080; BH1; 1. | | | |
| DR | PROSITE: PS01258; BH2; 1. | | | |
| DR | PROSITE: PS01260; BH4; 1; 1. | | | |
| DR | PROSITE: PS50063; BH4; 2; 1. | | | |
| SQ | SEQUENCE 219 AA; 23720 MW; 30E36041BCLDCE6F CRC64; | | | |
| Query Match | | | | |
| Best Local Similarity 98.9%; Score 996; DB 2; Length 219; | | | | |
| Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0 | | | | |
| QY | 1 NATPASAPDTRLVADFVGVGYKLRQGYVCGAPRGSPADPLHQMRAAGDEFETFRRT | 60 | | |
| DB | 27 MATPASTDTRLVADFGVGYKLRQGYVCGAPRGSPADPLHQMRAAGDEFETFRRT | 86 | | |
| QY | 61 FSDLAQLHTPTGSAQORFTQVSDLPFGGPNWGLVAFVFGALCAESVKNKEPVLG | 120 | | |
| DB | 87 FSDLAQLHTPTGSAQORFTQVSDLPFGGPNWGLVAFVFGALCAESVKNKEPVLG | 146 | | |
| QY | 121 QVQEMVAVYLETRLADWTHSSGGMNEPFLVGDGALREARLRRENNASVRYTLGVAAL | 180 | | |
| DB | 147 QVQDMVAVYLETRLADWTHSSGGMNEPFLVGDGALREARLRRENNASVRYTLGVAAL | 206 | | |
| QY | 181 GALTTVGAFPSK | 193 | | |
| DB | 207 GALTTVGAFPSK | 219 | | |
| RESULT 5 | | | | |
| ID | Q6A093 | PRELIMINARY; | PRT; | 192 AA. |
| AC | Q6A093; | | | |
| DT | 25-OCT-2004 (TrEMBLrel. 28, Created) | | | |
| DT | 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) | | | |
| DT | 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) | | | |
| DE | MKIA0271 protein (Fragment). | | | |
| DE | Name=MKIA0271; | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RP | SEQUENCE FROM N.A. | | | |

RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Iwamoto K., Ishii Y., Itoh M., Izawa M., Katsukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koyas K., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki K.,
RA Sogabe Y., Suzuki H., Tagami T., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AK013244; BAB28740.1; --
DR HSSP: Q92943; 100L.
DR MGD: MG1:108052; BCL212.
DR GO: GO:0016021; C:integral to membrane; TAS.
DR GO: GO:000515; F:protein binding; IPL.
DR GO: GO:0006915; P:apoptosis; IDA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BCL; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR PROSITE: PS00662; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS00663; BH4_2; 1.
DR PROSITE: PS00663; BH4_2; 1.
SQ SEQUENCE 178 AA; 19147 MW; E2D4C3F79528E9D7 CRC64;

Query Match 75.6%; Score 761; DB 2; Length 178;
Best Local Similarity 95.3%; Pred. No. 4,1e-60;
Matches 143; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MATPASPATRALVAADVGVYGLRQKGVYCGAPGEPGAADPLQAMPAAGDEPFPRT 60
Db 1 MATPASPATRALVAADVGVYGLRQKGVYCGAPGEPGAADPLQAMPAAGDEPFPRT 60
Qy 61 FSDIAAQLHTYTPGSAQORFTQVSELEFQGGPNMGRLVAFFVFAALCAESVKNEMPLVG 120
Db 61 FSDIAAQLHTYTPGSAQORFTQVSELEFQGGPNMGRLVAFFVFAALCAESVKNEMPLVG 120

Qy 121 QVQEWVAVLETRLADWTHSSGGAEPFAL 150
Db 121 QVQEWVAVLETRLADWTHSSGGAEPFAL 150
RESULT 9
ID Q6GP82 PRELIMINARY; PRT; 188 AA.
AC Q6GP82;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE MG80617 protein.
GN Name=MG80617;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
CX NCB1_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uddin T.B., Toehyuki S., Carninci P., Prange C.,
RA Raba S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McLean P.C., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz U., Myers R.M., Butterfield Y.S.,
RA Krzywnicki M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.V., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strauberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative.";
RL Dev. Dyn. 225:384-391(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC073259; AAH73259.1; --
DR GO: GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BCL; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR PROSITE: PS00662; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
SQ SEQUENCE 188 AA; 20441 MW; CB3C1A8C55F16B96 CRC64;

Query Match 64.7%; Score 651.5; DB 2; Length 188;

Best Local Similarity 68.9%; Pred. No. 2.8e-50;
Matches 126; Conservative 20; Mismatches 34; Indels 3; Gaps 1;

QY 11 RALVADPFGYKLRQKGYVCGAGPBGPAADPLHOAMRAAGDEFETRRRTSDLAQLHV 70
Db 9 RALVADPFGYKLRQKGYVCGAGPBGPAADPLHOAMRAAGDEFETRRRTSDLAQLHV 65
QY 71 TPQSAQORFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNKEMPELVQVQEMVAYL 130
Db 66 TPQSAQORFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNKEMPELVQVQEMVAYL 125
QY 131 ETRLADWHSNGMAEFTLYGDALEEARLRREGNMAVRYTLTGAVLGLVTVGAF 190
Db 126 ETRLADWHSNGMAEFTLYGDALEEARLRREGNMAVRYTLTGAVLGLVTVGAF 185
QY 191 ASK 193
Db 186 ASK 188

RESULT 10
ARI_XENLA STANDARD; PRT; 228 AA.

AC 091827;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator R1 (XR1) (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=95331613; PubMed=7607538; DOI=10.1016/0378-1119(95)00159-4;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RT cell-survival genes.";
RL Gene 158:171-179 (1995).
CC -1- FUNCTION: Could be the homolog of mammalian Bcl-W.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (potential).
CC -1- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the
CC brain of mid-metamorphic to post-metamorphic tadpoles and
CC adults, where an increase of several fold has been observed.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X82462; CA57845.1; -.
DR HSSP: Q07817; IMAZ.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR Apoptosis; Transmembrane.
FT NON_TER 1 1
FT DOMAIN 120 139 BH1.
FT DOMAIN 171 186 BH2.
FT TRANSMEM 207 227 Potential.

SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;

Query Match 64.2%; Score 646.5; DB 1; Length 228;
Best Local Similarity 67.9%; Pred. No. 9.6e-50;
Matches 125; Conservative 21; Mismatches 35; Indels 3; Gaps 1;

QY 10 TRALVADPFGYKLRQKGYVCGAGPBGPAADPLHOAMRAAGDEFETRRRTSDLAQLH 69
Db 48 SRALVELDVYKLCQRLV---PEPSGAASCALHSAMRAAGDEFETRRRTSDLAQLH 104
QY 70 VTPQSAQORFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNKEMPELVQVQEMVAY 129
Db 105 VTPQSAQORFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNKEMPELVQVQEMVAY 164
QY 130 LETRLADWHSNGMAEFTLYGDALEEARLRREGNMAVRYTLTGAVLGLVTVGAF 189
Db 165 LETRLADWHSNGMAEFTLYGDALEEARLRREGNMAVRYTLTGAVLGLVTVGAF 224
QY 190 FASK 193
Db 225 FASK 228

RESULT 11
Q9MYM4 PRELIMINARY; PRT; 233 AA.

AC Q9MYM4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bcl-X.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Knott J.C., Robertson L., James B.R.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY005131; AAF88137.1; -.
DR HSSP: P53563; IAF3.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PSS0063; BH4_2; 1.
SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

Query Match 43.7%; Score 440.5; DB 2; Length 233;
Best Local Similarity 42.0%; Pred. No. 2.7e-31;
Matches 94; Conservative 22; Mismatches 57; Indels 51; Gaps 4;

QY 11 RALVADPFGYKLRQKGYVCGAGPBGPAADPLHOAMRAAGDEFETRRRTSDLAQLHV 70
Db 6 RALVADPFGYKLRQKGYVCGAGPBGPAADPLHOAMRAAGDEFETRRRTSDLAQLHV 65
QY 40 D-----PLHOAMRAAGDEFETRRRTSDLAQLHVTPQSAQORFTQ 81
Db 66 NGATGHSLSLDAREVLPMTAVKQALREAGDEFELRYRARSDDLTSQHLITPGTAVGSFEO 125
QY 82 VSDLEFGGPNMGRVAFVFGAALCAESVKNKEMPELVQVQEMVAYLETRLADWHS 141

Db 126 VVNLFFDGVNMGVITVAFSGALCVESVDKEMEVLSRAAMATYLNHLEPMIGEN 185
 QY 142 GMAEFPALYDGDALBEARLRRE--GMAVRYTVLGTAVLALGAL 183
 Db 186 GMDTFVELYGNNAABSRKQCFRFRNFWLTGMTVAGVLLGSL 229

RESULT 12

Q8SQ42 PRELIMINARY; PRT; 233 AA.
 AC Q8SQ42; 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Bcl-x1 protein.
 GN Name=bcl-x1;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB080951; BAB85856.2; -
 DR HSSP; Q07817; IMAZ.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro; IPR000712; Bcl2 BH.
 DR InterPro; IPR003093; Bcl2 BH4.
 DR InterPro; IPR002475; Bcl2_family.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 SQ SEQUENCE 233 AA; 26017 MW; CD17F24FE9D47BC9 CRC64;
 Query Match 43.0%; Score 433.5; DB 2; Length 233;
 Best Local Similarity 41.6%; Pred. No. 1.1e-30;
 Matches 97; Conservative 23; Mismatches 58; Indels 55; Gaps 5;
 QY 11 RALVADPFGYKLRQKGY-----Y 28
 Db 6 RELVADFSTYKLSQKGSWSRPSDVEENRTEAPGTESEMETPSAINGNPSMHLADSPAV 65
 QY 29 CGAGRGEGEPAD-----PLHQMRAGDEFEFRFRTSDLAQLHTVPGSNOQRF 80
 Db 66 NGA-TGHSSSIDAREVIMAAVKQALRRAGSEFELRYRRAASDLTSQHITPGHYGSFE 124
 QY 81 QVSDLEFGQGNMGELVAFVFGAALCAESVKNKEMLPVGVQVQEWMAVYLETSLADWTHS 140
 Db 125 QVNVLEFRDGVNMGRIVAFSFGALCVESVDKEMQVLSRIAAAMATYLNHLEPMIGOE 184
 QY 141 SGMAEFPALYDGDALBEARLRREBNMAVTVLTGVALGALTVGAFPSK 193
 Db 185 NGMDTFVELYGNNAABSRK---QGRSRNMFVLTGMTVAG-VVLLGSLFSRK 233
 RESULT 13
 BCLX_CHICK STANDARD; PRT; 229 AA.
 AC Q07816; Q98908;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
 GN Name=BCL2L1; Synonyms=BCL-X, BCLX;
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RX MEDLINE=93364977; PubMed=8358789; DOI=10.1016/0092-8674(93)90508-N;
 RA Boise L.H., Gonzalez-Garcia M., Postema C.B., Ding L., Lindsten T.,
 RA Turkula L.A., Mao X., Nunez G., Thompson C.B.;
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator of
 RT apoptotic cell death.";
 RL Cell 74:597-608(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RC STRAIN=Hubbard White Mountain; TISSUE=Testis;
 RX MEDLINE=97264485; PubMed=9110311;
 RX DOI=10.1002/STCI.1098-2795(199705)47:1<26::AID-WRDA>3.3.CO;2-V;
 RA Viagrasa X., Mezquita C., Mezquita J.;
 RT "Differential expression of bcl-2 and bcl-x during chicken
 RT spermatogenesis.";
 RL Mol. Reprod. Dev. 47:26-29(1997).
 CC -1- FUNCTION: Dominant regulator of apoptotic cell death. The long
 CC form displays cell death repressor activity, whereas the short
 CC isoform promotes apoptosis (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
 CC envelope (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=long;
 CC IsoId=Q07816-1; Sequence=Displayed;
 CC Name=short;
 CC IsoId=Q07816-2; Sequence=VSP_000514;
 CC -1- TISSUE SPECIFICITY: Highest expression in organs with lymphoid
 CC development.
 CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
 CC function. Interact BH1 and BH2 domains are required for anti-
 CC apoptotic activity (By similarity).
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -----
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 CC -----
 CC EMBL; Z23110; CA80657.1; -
 CC EMBL; U26645; AAB07677.1; -
 CC PIR; A47537; A47537.
 DR HSSP; P53563; IAF3.
 DR InterPro; IPR000712; Bcl2 BH.
 DR InterPro; IPR003093; Bcl2 BH4.
 DR InterPro; IPR002475; Bcl2_family.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 KW Alternative splicing; Apoptosis; Transmembrane.

FT DOMAIN 4 24 BH4.
 FT DOMAIN 82 96 BH3.
 FT DOMAIN 125 144 BH1.
 FT TRANSSEM 176 191 BH2.
 FT TRANSSEM 206 223 Potential.
 FT VARSPLIC 185 229 ERFVLDYNNAAALRKQGTFFNKLVTGATVAGVLLGSL
 FT LSRK -> VRTALP (in isoform short).
 FT /FTId=VSP 000514.
 SQ SEQUENCE 229 AA; 25733 MW; A97DA4D04C0E9DA CRC64;

Query Match 42.9%; Score 432.5; DB 1; Length 229;
 Best Local Similarity 41.7%; Pred. No. 1.4e-30;
 Matches 95; Conservative 22; Mismatches 62; Indels 49; Gaps 4;

QY 11 RALVADPVGKLRKQKY-----VCGAGPEGP----- 37
 DB 6 RELVDFVSYKLRQRCWSELEEDENRTDTAAEMDSVLNGSPFMPHPAGHVNGAT 65
 QY 38 -----AADPLHQAARAGDEPFRFRFTFSDLAQLHTPGSAQOQFTQVSD 85
 DB 66 VRRSLEVEHIVASDVRLRDNGDEFELRRAFSDLTSLQHTTGTINQSFQVYNE 125
 QY 86 LFOGSPWGRVLVAFVFGALCAESVKNKEPVLGVQVQVEMVAVLETRLADWTHSSGMA 145
 DB 126 LPHDGVVWGRIVAFSFGALCVESVDKEMRVLGRIVSWMTTTLTDHLPWIGENGWE 185
 QY 146 EPTALYDGLAEARRLRKGNMWSVTVLTGAVAGLVTVGAFPAK 193
 DB 186 RFDVLYGNNA---AAELRKQGTFFNKLVTGATVAGVLL-IGSLSRK 229

RESULT 14
 BCLX_PIG STANDARD; PRT; 233 AA.
 ID BCLX_PIG 07737;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
 GN Name=BCL2L1; Synonyms=BCLX, BLC2L;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NC NCBL_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99171363; Pubmed=10072723; DOI=10.1006/jmcc.1998.0855;
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Diermer D.;
 RT "Quantification of cardioprotective gene expression in porcine short-term hibernating myocardium";
 RT J. Mol. Cell. Cardiol. 31:147-158 (1999).
 RL J. Mol. Cell. Cardiol. 31:147-158 (1999).
 CC -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-apoptotic activity is inhibited by association with SIVA isoform 1. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the voltage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome C, from the mitochondrial membrane.
 CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX, BAK and Bcl-2 (By similarity) required for anti-apoptotic activity (By similarity). Isoform Bcl-X(L) binds to Siva isoform 1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear envelope (By similarity).
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and Bcl-2 domains are required for both heterodimerization with other Bcl-2 family members and for repression of cell death.
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By similarity). The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (By similarity).
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ001203; CA004597.1; -.
 CC HSSP; Q07817; 1MAZ.
 CC InterPro; IPR000712; Bcl2_BH.
 CC InterPro; IPR003093; Bcl2_BH4.
 CC InterPro; IPR002475; Bcl2_family.
 CC InterPro; IPR004725; Bcl2_reg.
 CC Pfam; PF00452; Bcl1-2; 1.
 CC Pfam; PF02180; BH4; 1.
 CC TIGRFAMs; TIGR00865; bcl-2; 1.
 CC PROSITE; PS50062; BCL2_FAMILY; 1.
 CC PROSITE; PS01080; BH1; 1.
 CC PROSITE; PS01258; BH2; 1.
 CC PROSITE; PS01259; BH3; 1.
 CC PROSITE; PS01260; BH4; 1; 1.
 CC PROSITE; PS50063; BH4_2; 1.
 CC K0 Apoptosis; Mitochondrion; Transmembrane.
 FT DOMAIN 4 24 BH4.
 FT DOMAIN 86 100 BH3.
 FT DOMAIN 129 148 BH1.
 FT DOMAIN 180 195 BH2.
 FT TRANSSEM 210 226 Potential.
 SQ SEQUENCE 233 AA; 26061 MW; 18BF6A0441912B2 CRC64;

Query Match 42.9%; Score 431.5; DB 1; Length 233;
 Best Local Similarity 41.8%; Pred. No. 1.7e-30;
 Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADPVGKLRKQKY-----V 28
 DB 6 RELVDFVSYKLRQRCWSELEEDENRTDTAAEMDSVLNGSPFMPHPAGHVNGAT 65
 QY 29 CGAGPEGPAD-----PLHQAARAGDEPFRFRFTFSDLAQLHTPGSAQOQFT 80
 DB 66 NGA-TGHSSSLDAREVTPMAAVQALRENGDEFELRRAFSDLTSLQHTTGTINQSF 124
 QY 81 QVSDLEFQGGPWNKRLVAFVFGALCAESVKNKEPVLGVQVQVEMVAVLETRLADWTHS 140
 DB 125 QVNLDFRQGVNWRIVAFSFGALCVESVDKEMQVLSRIATWMTTTLTDHLPWIOE 184
 QY 141 SGWMAEFTALYDGLAEARRLRK--GNMWSVTVLTGAVAGLVTVGAFPAK 183
 DB 185 NGGMDTFVELYGNNAAESRKQGERFNRWFLTGMTLAGVLLGSL 229

RESULT 15
 Q9N1A2 PRELIMINARY; PRT; 233 AA.
 ID Q9N1A2
 AC Q9N1A2
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Anti-apoptotic regulator Bcl-XL.
 GN Name=bcl-xl;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NC NCBL_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Lee T.L., Cancy J.M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF216205; AAF33212.1; -.

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OM protein - protein search, using sw model

Run on: April 10, 2005, 20:12:38 ; Search time 65 Seconds
(without alignments)
1148.381 Million cell updates/sec

Title: US-09-925-674B-7

Perfect score: 1007

Sequence: 1 MATPAPAPDRFALVADPVG.....LTGAVLALGALVTGAPFASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 1007 | 100.0 | 193 | 2 | AAV05530 Human Bcl |
| 2 | 1007 | 100.0 | 193 | 7 | AdD46742 Human Bcl |
| 3 | 1007 | 100.0 | 193 | 8 | ADP88349 Human Bcl |
| 4 | 1002 | 99.5 | 193 | 2 | AAW61392 Human Bcl |
| 5 | 1002 | 99.5 | 193 | 2 | AAW97392 The human |
| 6 | 1000 | 99.3 | 193 | 2 | AAW36047 Human bcl |
| 7 | 1000 | 99.3 | 193 | 2 | AAV05532 Human Bcl |
| 8 | 1000 | 99.3 | 193 | 2 | AAV05531 Mouse Bcl |
| 9 | 997 | 99.0 | 192 | 2 | AAW97394 Mammalian |
| 10 | 996 | 98.9 | 193 | 2 | AAW61391 Rat bcl-y |
| 11 | 996 | 98.9 | 193 | 2 | AAW97391 The rat b |
| 12 | 991 | 98.4 | 192 | 2 | AAW97393 Protein b |
| 13 | 958.5 | 95.2 | 192 | 2 | AAV05533 Mouse Bcl |
| 14 | 954 | 94.7 | 183 | 8 | ADP88350 Derivative |
| 15 | 867 | 86.1 | 168 | 2 | AAW36048 Mouse bcl |
| 16 | 821.5 | 81.6 | 190 | 5 | AAO18223 Human Bcl |
| 17 | 766 | 76.1 | 365 | 2 | AAW58884 Amino aci |
| 18 | 766 | 76.1 | 365 | 5 | ABG95556 Human nov |
| 19 | 766 | 76.1 | 365 | 6 | ABO34750 Fragment |
| 20 | 766 | 76.1 | 365 | 7 | AD123411 Novel hum |
| 21 | 766 | 76.1 | 365 | 8 | ADH74413 Human sec |
| 22 | 764.5 | 75.9 | 185 | 8 | ABW84148 Human dia |
| 23 | 457.5 | 45.4 | 179 | 8 | ADH52635 Chinese h |
| 24 | 448.5 | 44.5 | 199 | 8 | ADH52637 Chinese h |
| 25 | 441.5 | 43.8 | 219 | 8 | ADH52639 Chinese h |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 26 | 436.5 | 43.3 | 219 | 8 | ADH52641 Chinese h |
| 27 | 435.5 | 43.0 | 342 | 8 | ADQ97763 Mouse can |
| 28 | 433.5 | 43.2 | 411 | 4 | AAU00219 Bcl-XL-DT |
| 29 | 431.5 | 42.9 | 233 | 4 | ADQ80679 Porcine a |
| 30 | 431.5 | 42.9 | 237 | 5 | ABG78480 Wild type |
| 31 | 429.5 | 42.7 | 233 | 8 | ADH52633 Chinese h |
| 32 | 428.5 | 42.6 | 233 | 2 | AAW05887 Human chy |
| 33 | 428.5 | 42.6 | 233 | 2 | AAW05882 Bcl-XL pr |
| 34 | 428.5 | 42.6 | 233 | 3 | AAW31530 Human ant |
| 35 | 428.5 | 42.6 | 233 | 3 | AAV59969 Human Bcl |
| 36 | 428.5 | 42.6 | 233 | 3 | AAV83223 Bcl-x pol |
| 37 | 428.5 | 42.6 | 233 | 4 | AAW50538 Human Bcl |
| 38 | 428.5 | 42.6 | 233 | 4 | AAW73303 Rat wild- |
| 39 | 428.5 | 42.6 | 233 | 4 | AAW64262 Human Bcl |
| 40 | 428.5 | 42.6 | 233 | 4 | AAW47515 Protein e |
| 41 | 428.5 | 42.6 | 233 | 7 | ADBE2921 Rat Prote |
| 42 | 428.5 | 42.6 | 233 | 7 | ADBE2493 Human Pro |
| 43 | 428.5 | 42.6 | 233 | 7 | ADBE2491 Rat Prote |
| 44 | 428.5 | 42.6 | 233 | 7 | ABW02410 Human bcl |
| 45 | 428.5 | 42.6 | 233 | 8 | ADW45995 Human apo |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | AAV05530 standard; protein; 193 AA. |
| ID | AAV05530 |
| XX | AAV05530; |
| AC | AAV05530; |
| XX | AAV05530; |
| DT | 05-JUL-1999 (first entry) |
| XX | 05-JUL-1999 (first entry) |
| DE | Human Bcl-w protein essential for spermatogenesis. |
| XX | Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility; |
| KW | animal model. |
| XX | animal model. |
| OS | Homo sapiens. |
| XX | Homo sapiens. |
| PN | WO9913710-A1. |
| XX | 25-MAR-1999. |
| PD | 25-MAR-1999. |
| PF | 16-SEP-1998; 98WO-AU000764. |
| XX | 16-SEP-1998; 98WO-AU000764. |
| PR | 16-SEP-1997; 97AU-00009228. |
| XX | 16-SEP-1997; 97AU-00009228. |
| PA | (HALT-) HALT INST MEDICAL RES WALTER & ELIZA. |
| XX | (HALT-) HALT INST MEDICAL RES WALTER & ELIZA. |
| PI | Cory J, Adams J, Print C, Gibson L, Koentgen F; |
| XX | Cory J, Adams J, Print C, Gibson L, Koentgen F; |
| DR | WPI; 1999-243890/20. |
| XX | WPI; 1999-243890/20. |
| PT | An animal model exhibiting reduced levels of a Bcl-w protein and/or |
| XX | protein associated with Bcl-w. |
| PS | Claim 2; Page 33; 52pp; English. |
| XX | Claim 2; Page 33; 52pp; English. |
| CC | The present sequence is human Bcl-w, a pro-survival member of the Bcl-2 |
| XX | family which is widely expressed and which is essential for |
| CC | spermatogenesis. The invention relates generally to a method of treatment |
| XX | and to an animal model for the identification of molecules and genetic |
| CC | sequences useful for inducing or reducing fertility of male animals. |
| XX | Methods are provided for the treatment of infertility, or for reducing |
| CC | fertility, by modulating spermatogenesis. An animal model carries a |
| XX | mutation in at least one allele of the human or murine bcl-w gene (see |
| CC | AXX25132-35) or in a gene associated with bcl-w. Such animals have |
| XX | disorganised seminiferous tubules and are substantially infertile, but |
| CC | possess no other major abnormalities as determined by histological |
| XX | examination. They can be used to screen for therapeutic molecules |
| CC | including genetic sequences capable of inducing, enhancing or otherwise |

CC facilitating spermatogenesis in animals, or which can induce infertility
XX Sequence 193 AA;
SQ

Query Match 100.0%; Score 1007; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.8e-102;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASPPTRALVADPVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETFRRT 60
DB 1 MATPASPPTRALVADPVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETFRRT 60
QY 61 FSDIAQLHVTTPGSAQOQRTQVSDDELFOGSPNMGRLVAFVFGAALCAESVNMKEPVLV 120
DB 61 FSDIAQLHVTTPGSAQOQRTQVSDDELFOGSPNMGRLVAFVFGAALCAESVNMKEPVLV 120
QY 121 QVQEMWVAYLETRLADWTHSSGMAEFTALYGDALAEARRLREGNMAVSRTVLTGAVAL 180
DB 121 QVQEMWVAYLETRLADWTHSSGMAEFTALYGDALAEARRLREGNMAVSRTVLTGAVAL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 2
ADP6742
ID ADD6742 standard; protein; 193 AA.
XX
AC ADD6742;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein Q92843, SEQ ID NO 12427.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SN1; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'Urso D, Befort K, Costigan M;
XX MPI; 2003-268312/26.
XX GENBANK; Q92843.
XX

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition,
CC a method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SN1) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPRO at
CC ftp.wipro.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 193 AA;
XX

Query Match 100.0%; Score 1007; DB 7; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.8e-102;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASPPTRALVADPVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETFRRT 60
DB 1 MATPASPPTRALVADPVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETFRRT 60
QY 61 FSDIAQLHVTTPGSAQOQRTQVSDDELFOGSPNMGRLVAFVFGAALCAESVNMKEPVLV 120
DB 61 FSDIAQLHVTTPGSAQOQRTQVSDDELFOGSPNMGRLVAFVFGAALCAESVNMKEPVLV 120
QY 121 QVQEMWVAYLETRLADWTHSSGMAEFTALYGDALAEARRLREGNMAVSRTVLTGAVAL 180
DB 121 QVQEMWVAYLETRLADWTHSSGMAEFTALYGDALAEARRLREGNMAVSRTVLTGAVAL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 3
ADP88349
ID ADP88349 standard; protein; 193 AA.
XX
AC ADP88349;
XX
DT 09-SEP-2004 (first entry)
DT 09-SEP-2004 (first entry)
XX
DE Human Bcl-w protein.
XX
KW Bcl-w; human; protein structure; protein co-ordinate data.
KW Homo sapiens.
XX
OS Homo sapiens.
XX
PN WO2004050697-A1.
XX
PD 17-JUN-2004.
XX
PF 03-DEC-2003; 2003WO-AU001624.
XX
PR 03-DEC-2002; 2002AU-00953259.
XX
PA (HALI-) HALI INST MEDICAL RES WALTER & ELIZA.
XX
PI Hinds MG, Huang DCS, Day CL;
XX MPI; 2004-487529/46.
XX
XX Solution useful for identifying or selecting agents that are capable of

inhibiting biological activity of Bcl-w, comprises molecule that has Bcl-w active site defined by specific structure coordinates of Bcl-w amino acid residues.

Disclousure; Page 804-805; 810pp; English.

The present invention relates to a solution comprising a molecule or molecular complex that comprises at least a fragment of Bcl-w. Also disclosed is the structure of Bcl-w, in the form of protein coordinate data. The solution is useful for identifying, selecting or designing agents that are capable of inhibiting or potentiating one or more biological activity of Bcl-w, and in solving the structures of other proteins with similar structure. It is also useful for characterizing the three-dimensional structure of the Bcl-w molecule, molecular complex or its derivative. The present sequence is the human Bcl-w protein.

Sequence 193 AA;

Query Match 100.0%; Score 1007; DB 8; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.8e-102;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASADPTRALVADPVGYKLRQGYVCGAPGEGPADPLHQAAMRAAGDEFETRRRT 60
DB 1 MATPASADPTRALVADPVGYKLRQGYVCGAPGEGPADPLHQAAMRAAGDEFETRRRT 60
QY 61 FSDLAQLHTTPGSAOQRFQVSDLEFGGPNMGRVAFVFGAALCAESVNKEMEPLVG 120
DB 61 FSDLAQLHTTPGSAOQRFQVSDLEFGGPNMGRVAFVFGAALCAESVNKEMEPLVG 120
QY 121 QVQEMWVAYLETRLADWTHSSGNAEFTALYGDALBEARLRBGNMASVRTVLTGAVAL 180
DB 121 QVQEMWVAYLETRLADWTHSSGNAEFTALYGDALBEARLRBGNMASVRTVLTGAVAL 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193

RESULT 4
ID AAW61392 standard; protein; 193 AA.

AC AAW61392;
XX
DT 02-OCT-1998 (first entry)
XX
DE Human bcl-y protein.
XX
KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
XX
OS Homo sapiens.
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-00798897.
XX
PR 23-FEB-1996; 96US-0012201P.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1998-446079/38.
XX
DR N-PSDB; AAV28334.
XX
PT Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g. cancers.
XX
PS Example; Column 17/18; 27pp; English.

XX The mammalian bcl-y protein is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired

Sequence 193 AA;

Query Match 99.5%; Score 1002; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 6.6e-102;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASADPTRALVADPVGYKLRQGYVCGAPGEGPADPLHQAAMRAAGDEFETRRRT 60
DB 1 MATPASADPTRALVEDPVGYKLRQGYVCGAPGEGPADPLHQAAMRAAGDEFETRRRT 60
QY 61 FSDLAQLHTTPGSAOQRFQVSDLEFGGPNMGRVAFVFGAALCAESVNKEMEPLVG 120
DB 61 FSDLAQLHTTPGSAOQRFQVSDLEFGGPNMGRVAFVFGAALCAESVNKEMEPLVG 120
QY 121 QVQEMWVAYLETRLADWTHSSGNAEFTALYGDALBEARLRBGNMASVRTVLTGAVAL 180
DB 121 QVQEMWVAYLETRLADWTHSSGNAEFTALYGDALBEARLRBGNMASVRTVLTGAVAL 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193

RESULT 5
ID AAW97392 standard; protein; 193 AA.

AC AAW97392;
XX
DT 20-MAY-1999 (first entry)
XX
DE The human bcl-y protein.
XX
KW Rat bcl-y protein; Bbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS Homo sapiens.
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-00978523.
XX
PR 23-FEB-1996; 96US-0012201P.
XX
PR 11-FEB-1997; 97US-00798897.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
XX
DR N-PSDB; AAX15946.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death.
XX
PS Claim 1; Col 17-18; 26pp; English.

XX The present sequence represents human bcl-y protein (Hbcl-y). The
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-
CC y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and
CC Hbcl-y may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites
XX
SQ Sequence 193 AA;

Query Match 99.5%; Score 1002; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 6 6e-102;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADVFVGKLRQKGYVCGAGBEGSPADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASAPDTRALVADVFVGKLRQKGYVCGAGBEGSPADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDIAAQLHVTPESSAQORFTQVSDDELFOGSPMNGRLVAFVFGALCAESVNKEMEPLVG 120
DB 61 FSDIAAQLHVTPESSAQORFTQVSDDELFOGSPMNGRLVAFVFGALCAESVNKEMEPLVG 120
QY 121 QVQEMWVALETRLDWIIHSSGMAEFTALYGDGALBEARLRREGNMASVRTLGAVAL 180
DB 121 QVQEMWVALETRLDWIIHSSGMAEFTALYGDGALBEARLRREGNMASVRTLGAVAL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 6
AAW36047
ID AAW36047 standard; protein; 193 AA.
AC AAW36047;
XX
XX
DT 22-APR-1998 (first entry)
DE Human bcl-w protein.
XX
XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease.
XX
OS Homo sapiens.
XX
FN WO9735971-A1.
XX
PD 02-OCT-1997.
XX
PF 27-MAR-1997; 97WO-AU000199.
XX
PR 27-MAR-1996; 96AU-00008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Cory S, Adams JM, Gibson LM, Holmgreen SP;
XX WPI; 1997-489635/45.
DR N-PSDB; AAT96577.
XX

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
PT inhibit cell survival, e.g. for treatment of cancer and degenerative
XX diseases.
PS Claim 6; Page 48; 86pp; English.

XX This sequence represents a novel human protein, bcl-w, encoded by the bcl
CC -2 gene family and extracted from an adult brain library. This gene
CC promotes cell survival, so its modulation is useful in treatment of
CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
CC ischaemia, human immunodeficiency virus infection or in cell transplants.
CC Up-regulation of the gene can also be used to modify cell lines cultured
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
CC and to increase survival of primary explants during genetic modification.
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
XX antibody production or screening of potential modulators

SQ Sequence 193 AA;

Query Match 99.3%; Score 1000; DB 2; Length 193;
Best Local Similarity 99.0%; Pred. No. 1.1e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADVFVGKLRQKGYVCGAGBEGSPADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASAPDTRALVADVFVGKLRQKGYVCGAGBEGSPADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDIAAQLHVTPESSAQORFTQVSDDELFOGSPMNGRLVAFVFGALCAESVNKEMEPLVG 120
DB 61 FSDIAAQLHVTPESSAQORFTQVSDDELFOGSPMNGRLVAFVFGALCAESVNKEMEPLVG 120
QY 121 QVQEMWVALETRLDWIIHSSGMAEFTALYGDGALBEARLRREGNMASVRTLGAVAL 180
DB 121 QVQEMWVALETRLDWIIHSSGMAEFTALYGDGALBEARLRREGNMASVRTLGAVAL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 7
AA05532
ID AA05532 standard; protein; 193 AA.
AC AA05532;
XX
XX
DT 05-JUL-1999 (first entry)
DE Human Bcl-w protein essential for spermatogenesis.
XX
XX Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW animal model.
XX
OS Homo sapiens.
XX
FN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX WPI; 1999-243890/20.
DR N-PSDB; AAX25134.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.

XX Disclosure, Page 37, 52pp; English.

CC The present sequence is described of a derivative of human Bcl-w (see
CC also AAY05530), a pro-survival member of the Bcl-2 family that is widely
CC expressed and which is essential for spermatogenesis. The invention
CC relates generally to a method of treatment and to an animal model for the
CC identification of molecules and genetic sequences useful for inducing or
CC reducing fertility of male animals. Methods are provided for the
CC treatment of infertility, or for reducing fertility, by modulating
CC spermatogenesis. An animal model carries a mutation is at least one
CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
CC associated with bcl-w. Such animals have disorganised seminiferous tubules
CC and are substantially infertile, but possess no other major abnormalities
CC as determined by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of inducing,
CC enhancing or otherwise facilitating spermatogenesis in animals, or which
CC can induce infertility

XX Sequence 193 AA;

Query Match 99.3%; Score 1000; DB 2; Length 193;
Best Local Similarity 99.0%; Pred. No. 1.1e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGPBGPAADPLHQAMPAGDEFETRRRT 60
DB 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGPBGPAADPLHQAMPAGDEFETRRRT 60
QY 61 FSDLAQLHTVTPGSAOQRFQVSDDELFOGSPNNRGLVAFVFGAALCAESVNMKEPLVG 120
DB 61 FSDLAQLHTVTPGSAOQRFQVSDDELFOGSPNNRGLVAFVFGAALCAESVNMKEPLVG 120
QY 121 QVQEMWVAVYETRLADWIHSSGGWAEFTALYGDALBEARLRBGWNASVRYTLTGAVAL 180
DB 121 QVQEMWVAVYETRLADWIHSSGGWAEFTALYGDALBEARLRBGWNASVRYTLTGAVAL 180
QY 181 GALVTGAFPPASK 193
DB 181 GALVTGAFPPASK 193

RESULT 8
AAY05531

ID AAY05531 standard; protein; 193 AA.

XX AAY05531;

DT 05-JUL-1999 (first entry)

DE Mouse Bcl-w protein essential for spermatogenesis.

KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW animal model.

OS Mus sp.

PN W09913710-A1.

PD 25-MAR-1999.

PF 16-SEP-1998; 98WC-AU000764.

PR 16-SEP-1997; 97AU-00009228.

PA (HALT-) HALT INST MEDICAL RES WALTER & ELIZA.

PI Cory S, Adams J, Print C, Gibson L, Koentgen F;

DR WPI, 1999-243890/20.

DR N-PSDB; AAX25133.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or

PT protein associated with Bcl-w.

XX Claim 2; Page 35; 52pp; English.

CC The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2
CC family which is widely expressed and which is essential for
CC spermatogenesis. The invention relates generally to a method of treatment
CC and to an animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for reducing
CC fertility, by modulating spermatogenesis. An animal model carries a
CC mutation is at least one allele of the human or murine bcl-w gene (see
CC AAX25132-35) or in a gene associated with bcl-w. Such animals have
CC disorganised seminiferous tubules and are substantially infertile, but
CC possess no other major abnormalities as determined by histological
CC examination. They can be used to screen for therapeutic molecules
CC including genetic sequences capable of inducing, enhancing or otherwise
CC facilitating spermatogenesis in animals, or which can induce infertility

XX Sequence 193 AA;

Query Match 99.3%; Score 1000; DB 2; Length 193;
Best Local Similarity 99.0%; Pred. No. 1.1e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGPBGPAADPLHQAMPAGDEFETRRRT 60
DB 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGPBGPAADPLHQAMPAGDEFETRRRT 60
QY 61 FSDLAQLHTVTPGSAOQRFQVSDDELFOGSPNNRGLVAFVFGAALCAESVNMKEPLVG 120
DB 61 FSDLAQLHTVTPGSAOQRFQVSDDELFOGSPNNRGLVAFVFGAALCAESVNMKEPLVG 120
QY 121 QVQEMWVAVYETRLADWIHSSGGWAEFTALYGDALBEARLRBGWNASVRYTLTGAVAL 180
DB 121 QVQEMWVAVYETRLADWIHSSGGWAEFTALYGDALBEARLRBGWNASVRYTLTGAVAL 180
QY 181 GALVTGAFPPASK 193
DB 181 GALVTGAFPPASK 193

RESULT 9
AAM97394

ID AAM97394 standard; protein; 192 AA.

XX AAM97394;

DT 20-MAY-1999 (first entry)

DE Mammalian bcl-y protein.

KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.

OS Mammalia.

PN US5883229-A.

PD 16-MAR-1999.

PF 25-NOV-1997; 97US-00978523.

PR 23-FEB-1996; 96US-0012201P.

PR 11-FEB-1997; 97US-00798897.

PA (COCE-) COCENSYS INC.

PI Guastella J;
 XX
 DR WPI; 1999-214150/18.
 XX
 PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
 XX modulating programmed cell death.
 PS Claim 2; Col 19-22; 26pp; English.
 CC
 CC The present sequence represents a mammalian bcl-2 protein. The
 CC specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
 CC thought to be involved in programmed cell death (apoptosis and necrosis).
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
 CC with a disruption of the cell death pathway. If they act as cell death
 CC inhibitors, they may be used in therapies to treat subjects suffering
 CC from strokes, head trauma, Alzheimer's Disease, neural and muscular
 CC degenerative diseases (especially multiple sclerosis), myocardial
 CC infarction, vitally induced cell death, aging, spinal cord injuries and
 CC amyotrophic lateral sclerosis - conditions where cells under go premature
 CC cell death as a result of triggers which may or may not be apparent. They
 CC may also be used in this way to develop cell lines which remain viable in
 CC culture for an extended period. In contrast, if they act as cell death
 CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated
 CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma
 CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites
 XX
 SQ Sequence 192 AA;

Query Match 99.0%; Score 997; DB 2; Length 192;
 Best Local Similarity 99.5%; Pred. No. 2.3e-101;
 Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ATPASAPDTRALVADFGYKLRQGYCGAGPBGSGPADLHQAMRAAGDEFETFRRT 61
 Db 1 ATPASAPDTRALVADFGYKLRQGYCGAGPBGSGPADLHQAMRAAGDEFETFRRT 61
 QY 62 SDLAQLHVTGSAQOQRTQVSDLEFQGGPNMGRVAFVFGALCASVKNKEEPLVG 60
 Db 61 SDLAQLHVTGSAQOQRTQVSDLEFQGGPNMGRVAFVFGALCASVKNKEEPLVG 60
 QY 122 VOEMWAVYLETRLADWTHSSGMAEFTALYGDALAEARLRREGWASVRTLGAVALG 120
 Db 121 VOEMWAVYLETRLADWTHSSGMAEFTALYGDALAEARLRREGWASVRTLGAVALG 181
 QY 182 ALVTGAFPFASK 193
 Db 181 ALVTGAFPFASK 192

RESULT 10
 AAM61391
 ID AAM61391 standard; protein; 193 AA.
 XX
 AC AAM61391;
 XX
 DT 02-OCT-1998 (first entry)
 XX
 DE Rat bcl-y protein.
 XX
 KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
 OS Rattus sp.
 XX
 PN US5789201-A.
 XX
 PD 04-AUG-1998.
 XX
 PF 11-FEB-1997; 97US-00798897.
 XX
 PR 23-FEB-1996; 96US-0012201P.
 XX

PA (COCE-) COCENSYS INC.
 XX
 PI Guastella J;
 XX
 DR WPI; 1998-446079/38.
 XX
 DR N-PSDB; AAV28333.
 XX
 PT Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing
 XX recombinant protein for use in treating uncontrolled cell growth e.g.
 PS cancers.
 CC Example; Fig 3A; 27pp; English.
 CC
 CC The mammalian bcl-y protein is a member of the bcl-2 family, components
 CC of the cell death pathway. The bcl-2 family have both apoptotic activity
 CC and the apoptosis blocking activity. bcl-y falls in the apoptosis
 CC activity category. The recombinant protein may be used to prevent
 CC uncontrolled cell growth, either by its direct administration to
 CC recombinant genetic constructs to increase its expression in vivo. Also,
 CC antisense constructs can be used in disorders where prevention of cell
 CC death is desired
 XX
 SQ Sequence 193 AA;

Query Match 98.9%; Score 996; DB 2; Length 193;
 Best Local Similarity 98.4%; Pred. No. 3e-101;
 Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MATPASAPDTRALVADFGYKLRQGYCGAGPBGSGPADLHQAMRAAGDEFETFRRT 60
 Db 1 MATPASAPDTRALVADFGYKLRQGYCGAGPBGSGPADLHQAMRAAGDEFETFRRT 60
 QY 61 FSDLAQLHVTGSAQOQRTQVSDLEFQGGPNMGRVAFVFGALCASVKNKEEPLVG 120
 Db 61 FSDLAQLHVTGSAQOQRTQVSDLEFQGGPNMGRVAFVFGALCASVKNKEEPLVG 120
 QY 121 VOEMWAVYLETRLADWTHSSGMAEFTALYGDALAEARLRREGWASVRTLGAVAL 180
 Db 121 VOEMWAVYLETRLADWTHSSGMAEFTALYGDALAEARLRREGWASVRTLGAVAL 180
 QY 181 GALVTGAFPFASK 193
 Db 181 GALVTGAFPFASK 193

RESULT 11
 AAM97391
 ID AAM97391 standard; protein; 193 AA.
 XX
 AC AAM97391;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE The rat bcl-y protein.
 XX
 KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
 OS Rattus sp.
 XX
 PN US5683229-A.
 XX
 PD 16-MAR-1999.
 XX
 PF 25-NOV-1997; 97US-00978523.
 XX
 PR 23-FEB-1996; 96US-0012201P.
 XX
 PR 11-FEB-1997; 97US-00798897.
 XX

XX (COCE-) COCENSYS INC.
 PA Guastella J;
 PI WPI: 1999-214150/18.
 XX DR N-PSDB; AAX15945.
 XX
 PT Novel bcl-2 protein homologues of the rat and human bcl-2 protein - useful for
 PT modulating programmed cell death.
 XX
 PS Disclosure; Col 15-18; 26pp; English.
 XX
 CC The present sequence represents rat bcl-2 protein (Rbcl-2). The
 CC specification also describes human bcl-2 protein (Hbcl-2). Rbcl-2 and
 CC Hbcl-2 are homologues of the bcl-2 protein thought to be involved in
 CC programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2
 CC proteins may be used to treat conditions associated with a disruption of
 CC the cell death pathway. If they act as cell death inhibitors, they may be
 CC used in therapies to treat subjects suffering from: strokes, head trauma,
 CC Alzheimer's Disease, neural and muscular degenerative diseases
 CC (especially multiple sclerosis), myocardial infarction, vitally induced
 CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
 CC - conditions where cells under go premature cell death as a result of
 CC triggers which may or may not be apparent. They may also be used in this
 CC way to develop cell lines which remain viable in culture for an extended
 CC period. In contrast, if they act as cell death stimulators, Rbcl-2 and
 CC Hbcl-2 may be used to treat conditions associated with prolonged cell
 CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)
 CC and auto/hyperimmune diseases. They may also be used to cause cell death
 CC in, and hence control, parasites
 XX
 SQ Sequence 193 AA;
 Query Match 98.9%; Score 996; DB 2; Length 193;
 Best Local Similarity 98.4%; Pred. No. 3e-101;
 Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MATPASAPDTRALVADVGVYKLRQGYVCGAPGEGPAADPLHQMRAAGDEFFTRFRRT 60
 DB 1 MATPASAPDTRALVADVGVYKLRQGYVCGAPGEGPAADPLHQMRAAGDEFFTRFRRT 60
 QY 61 FSDLAAGLHTVTPGSAQOQFTQVSDLELFOGGPNMGRGLVAFVFGAALCAESYNKKEBPLVQ 120
 DB 61 FSDLAAGLHTVTPGSAQOQFTQVSDLELFOGGPNMGRGLVAFVFGAALCAESYNKKEBPLVQ 120
 QY 121 QVQEMWVAVYLETRLADWIHSSGNAEFPTALYGDGALBEARLRREGNMASVATVLTGAVAL 180
 DB 121 QVQEMWVAVYLETRLADWIHSSGNAEFPTALYGDGALBEARLRREGNMASVATVLTGAVAL 180
 QY 181 GALVTGAFPAASK 193
 DB 181 GALVTGAFPAASK 193
 RESULT 12
 ID AAM97393 standard; protein; 192 AA.
 XX AAM97393;
 AC
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE Protein sequence of the specification.
 XX
 KM Rat bcl-2 protein; Rbcl-2; human bcl-2 protein; Hbcl-2; bcl-2 homologue;
 KM programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KM head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KM multiple sclerosis; myocardial infarction; vitally induced cell death;
 KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KM premature cell death; cell death stimulator; prolonged cell life span;
 KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
 XX

OS Unidentified.
 XX
 XX US583229-A.
 XX
 XX 16-MAR-1999.
 XX
 PD 25-NOV-1997; 97US-00978523.
 PF
 XX 23-FEB-1996; 96US-0012201P.
 PR 11-FEB-1997; 97US-00798897.
 XX
 XX (COCE-) COCENSYS INC.
 PA Guastella J;
 PI WPI: 1999-214150/18.
 XX
 PT Novel bcl-2 protein homologues of the rat and human bcl-2 protein - useful for
 PT modulating programmed cell death.
 XX
 PS Disclosure; Col 19-20; 26pp; English.
 XX
 CC The specification describes rat bcl-2 protein (Rbcl-2) and human bcl-2
 CC protein (Hbcl-2). Rbcl-2 and Hbcl-2 are homologues of the bcl-2 protein
 CC thought to be involved in programmed cell death (apoptosis and necrosis).
 CC Rbcl-2 and Hbcl-2 proteins may be used to treat conditions associated
 CC with a disruption of the cell death pathway. If they act as cell death
 CC inhibitors, they may be used in therapies to treat subjects suffering
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
 CC degenerative diseases (especially multiple sclerosis), myocardial
 CC infarction, vitally induced cell death, aging, spinal cord injuries and
 CC amyotrophic lateral sclerosis - conditions where cells under go premature
 CC cell death as a result of triggers which may or may not be apparent. They
 CC may also be used in this way to develop cell lines which remain viable in
 CC culture for an extended period. In contrast, if they act as cell death
 CC stimulators, Rbcl-2 and Hbcl-2 may be used to treat conditions associated
 CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma
 CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites
 XX
 SQ Sequence 192 AA;
 Query Match 98.4%; Score 991; DB 2; Length 192;
 Best Local Similarity 98.4%; Pred. No. 1.1e-100;
 Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 ATPASAPDTRALVADVGVYKLRQGYVCGAPGEGPAADPLHQMRAAGDEFFTRFRRT 61
 DB 1 ATPASAPDTRALVADVGVYKLRQGYVCGAPGEGPAADPLHQMRAAGDEFFTRFRRT 60
 QY 62 SDLAAGLHTVTPGSAQOQFTQVSDLELFOGGPNMGRGLVAFVFGAALCAESYNKKEBPLVQ 121
 DB 61 SDLAAGLHTVTPGSAQOQFTQVSDLELFOGGPNMGRGLVAFVFGAALCAESYNKKEBPLVQ 120
 QY 122 QVQEMWVAVYLETRLADWIHSSGNAEFPTALYGDGALBEARLRREGNMASVATVLTGAVAL 181
 DB 122 QVQEMWVAVYLETRLADWIHSSGNAEFPTALYGDGALBEARLRREGNMASVATVLTGAVAL 180
 QY 181 ALVTGAFPAASK 193
 DB 181 ALVTGAFPAASK 192
 RESULT 13
 ID AAY05533 standard; protein; 192 AA.
 XX AAY05533;
 AC
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Mouse Bcl-2 protein derivative.
 XX

KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
 KW animal model.
 OS Mus sp.
 PN WO9913710-A1.
 XX 25-MAR-1999.
 PD 16-SEP-1998; 98WO-AU000764.
 PF 16-SEP-1997; 97AU-00009228.
 PR 16-SEP-1997; 97AU-00009228.
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA Cory S, Adams J, Print C, Gibson L, Koentgen F;
 PI WPI, 1999-243890/20.
 DR N-PSDB; AAX25135.
 XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 PS Disclosure; Page 39; 52pp; English.
 XX The present sequence is described of a derivative of mouse Bcl-w (see
 CC also AAY05531), a pro-survival member of the Bcl-2 family that is widely
 CC expressed and which is essential for spermatogenesis. The derivative
 CC lacks the 24 N-terminal amino acids of Bcl-w. The invention relates
 CC generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation at least one
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
 CC associated with bcl-w. Such animals have disorganized seminiferous tubules
 CC and are substantially infertile, but possess no other major abnormalities
 CC as determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility
 CC
 SO Sequence 192 AA;
 Query Match 95.2%; Score 958.5; DB 2; Length 192;
 Best Local Similarity 94.8%; Pred. No. 4.1e-97;
 Matches 183; Conservative 6; Mismatches 3; Indels 1; Gaps 1;
 QY 1 MATPASAPDTRALVADPVGKLRQKGYCGAGPGEPPADPLHQAARAGDEFETRRRT 60
 DB 1 MPTPASTPDRALVADPVGKLRQKGYCGAGPGEPPADPLHQAARAGDEFETRRRT 60
 QY 61 FSDLAALQHTVTPGSAQORFTQVSDDELFOGPGNMGRLVAFVFGAALCAESVNKMEPLVG 120
 DB 61 FSDLAALQHTVTPGSAQORFTQVSDDELFOGPGNMGRLVAFVFGAALCAESVNKMEPLVG 120
 QY 121 QVQEMWVAVLETRLDWTHSSGGWAEFTALYGDGALBEARRLREGNMAVTRVLGVAL 180
 DB 121 QVQEMWVAVLETRLDWTHSSGGWAEFTALYGDGALBEARRLREGNMAVTRVLGVAL 180
 QY 181 GALVTGGAFFASK 193
 DB 181 GALVTGGAFFASK 192
 RESULT 14
 ADP88350
 ID ADP88350 standard; protein; 183 AA.
 XX
 AC ADP88350;
 XX
 DT 09-SEP-2004 (first entry)
 XX

DE Derivative of human Bcl-w protein.
 XX Bcl-w; human; protein structure; protein co-ordinate data; mutant;
 KW muclein.
 OS Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 128 /note= "wild-type Ala substituted by Glu"
 FT WO2004050697-A1.
 XX 17-JUN-2004.
 PD 03-DEC-2003; 2003WO-AU001624.
 PF 03-DEC-2002; 2002AU-00953259.
 PR (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA Hinds MG, Huang DCS, Day CL;
 PI WPI, 2004-487529/46.
 DR Solution useful for identifying or selecting agents that are capable of
 XX inhibiting biological activity of Bcl-w, comprises molecule that has Bcl-
 PT w active site defined by specific structure coordinates of Bcl-w amino
 PT acid residues.
 PS Claim 16; Page 805-806; 810pp; English.
 XX The present invention relates to a solution comprising a molecule or
 CC molecular complex that comprises at least a fragment of Bcl-w. Also
 CC disclosed is the structure of Bcl-w, in the form of protein coordinate
 CC data. The solution is useful for identifying, selecting or designing
 CC agents that are capable of inhibiting or potentiating one or more
 CC biological activity of Bcl-w, and in solving the structures of other
 CC proteins with similar structure. It is also useful for characterizing the
 CC three-dimensional structure of the Bcl-w molecule, molecular complex or
 CC its derivative. The present sequence is a derivative of the human Bcl-w
 CC protein.
 CC
 SO Sequence 183 AA;
 Query Match 94.7%; Score 954; DB 8; Length 183;
 Best Local Similarity 99.5%; Pred. No. 1.2e-96;
 Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MATPASAPDTRALVADPVGKLRQKGYCGAGPGEPPADPLHQAARAGDEFETRRRT 60
 DB 1 MATPASAPDTRALVADPVGKLRQKGYCGAGPGEPPADPLHQAARAGDEFETRRRT 60
 QY 61 FSDLAALQHTVTPGSAQORFTQVSDDELFOGPGNMGRLVAFVFGAALCAESVNKMEPLVG 120
 DB 61 FSDLAALQHTVTPGSAQORFTQVSDDELFOGPGNMGRLVAFVFGAALCAESVNKMEPLVG 120
 QY 121 QVQEMWVAVLETRLDWTHSSGGWAEFTALYGDGALBEARRLREGNMAVTRVLGVAL 180
 DB 121 QVQEMWVAVLETRLDWTHSSGGWAEFTALYGDGALBEARRLREGNMAVTRVLGVAL 180
 QY 181 GAL 183
 DB 181 GAL 183
 RESULT 15
 AAM36048
 ID AAM36048 standard; protein; 168 AA.
 XX
 AC AAM36048;
 XX

DT 22-APR-1998 (first entry)

XX Mouse bcl-w protein.

DE Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 KW diagnosis; degenerative disease.

XX Mus ap.

XX WO9735971-A1.

XX 02-OCT-1997.

XX 27-MAR-1997; 97WO-AU000199.

XX 27-MAR-1996; 96AU-00008965.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Cory S, Adams JM, Gibson LM, Holmgren SP;

XX WPI; 1997-489635/45.

XX N-PSDB; AAT96578.

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
 inhibit cell survival, e.g. for treatment of cancer and degenerative
 diseases.

XX Claim 6; Page 50-51; 86pp; English.

CC This sequence represents a novel protein, bcl-w, encoded by the mouse bcl-
 -2 gene family. This gene promotes cell survival, so its modulation is
 useful in treatment of cancer or auto-immune diseases, degenerative
 diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular
 degeneration, hypoxia, ischaemia, human immunodeficiency virus infection
 or in cell transplants. Up-regulation of the gene can also be used to
 modify cell lines cultured in vivo, e.g. to develop new lines, to
 facilitate isolation of hybridomas and to increase survival of primary
 explants during genetic modification. It can be used to produce
 recombinant Bcl-w for therapy, diagnosis, antibody production or
 screening of potential modulators

XX Sequence 168 AA;

Query Match 86.1%; Score 867; DB 2; Length 168;

Best Local Similarity 95.8%; Pred. No. 4.3e-87;
 Matches 161; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAADPRALVADPVGYKLRQGYVCGAGPGSPADPLHQAMRAAGDEPFRRT 60

DB 1 MPTPASTPDRALVADPVGYKLRQGYVCGAGPGSPADPLHQAMRAAGDEPFRRT 60

QY 61 FSDLAALQHTVPGSAQORFTQVSDLEFGGPNMGRIVAFFVFGAALCAESVKNKEMEPLVG 120

DB 61 FSDLAALQHTVPGSAQORFTQVSDLEFGGPNMGRIVAFFVFGAALCAESVKNKEMEPLVG 120

QY 121 QVOBEMVAVYLETRIADWIHSSGGWAEFTALYGDALBEARRLRGNWA 168

DB 121 QVQDMIVAVYLETRIADWIHSSGGWAEFTALYGDALBEARRLRGNWA 168

Search completed: April 10, 2005, 22:40:49
 Job time : 68 secs

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OM protein - protein search, using sw model

Run on: April 10, 2005, 22:43:04 ; Search time 227.5 Seconds

(without alignments)
281.650 Million cell updates/sec

Title: US-09-925-674B-7

Perfect score: 1007
Sequence: 1 MATPASPDRALVADPVG.....LTGVALGALVTGAFRASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 1007 | 100.0 | 193 | 9 | US-09-925-674A-7 |
| 2 | 1007 | 100.0 | 193 | 16 | US-10-450-366-6 |
| 3 | 997 | 99.0 | 193 | 9 | US-09-925-674A-7 |
| 4 | 766 | 76.1 | 365 | 10 | US-09-809-391-696 |
| 5 | 766 | 76.1 | 365 | 10 | US-09-882-171-696 |
| 6 | 766 | 76.1 | 365 | 15 | US-10-164-861-696 |
| 7 | 627.5 | 62.3 | 228 | 16 | US-10-659-705-2 |
| 8 | 457.5 | 45.4 | 179 | 15 | US-10-402-017-6 |
| 9 | 448.5 | 44.5 | 199 | 15 | US-10-402-017-8 |
| 10 | 441.5 | 43.8 | 219 | 15 | US-10-402-017-10 |
| 11 | 436.5 | 43.3 | 219 | 15 | US-10-402-017-12 |
| 12 | 433.5 | 43.0 | 411 | 16 | US-10-792-517-2 |
| 13 | 432.5 | 42.9 | 229 | 16 | US-10-659-705-7 |

| | | | | | | |
|----|-------|------|-----|----|--------------------|--------------------|
| 14 | 429.5 | 42.7 | 233 | 15 | US-10-402-017-4 | Sequence 4, Appl1 |
| 15 | 428.5 | 42.6 | 233 | 9 | US-09-734-846-2 | Sequence 2, Appl1 |
| 16 | 428.5 | 42.6 | 233 | 9 | US-09-952-278-6 | Sequence 6, Appl1 |
| 17 | 428.5 | 42.6 | 233 | 14 | US-10-101-482-14 | Sequence 14, Appl1 |
| 18 | 428.5 | 42.6 | 233 | 14 | US-10-072-830-4 | Sequence 4, Appl1 |
| 19 | 428.5 | 42.6 | 233 | 14 | US-10-169-223-10 | Sequence 10, Appl1 |
| 20 | 428.5 | 42.6 | 233 | 14 | US-10-302-262-2 | Sequence 2, Appl1 |
| 21 | 428.5 | 42.6 | 233 | 15 | US-10-116-275-171 | Sequence 171, App |
| 22 | 428.5 | 42.6 | 233 | 16 | US-10-450-366-5 | Sequence 5, Appl1 |
| 23 | 428.5 | 42.6 | 233 | 16 | US-10-659-705-8 | Sequence 8, Appl1 |
| 24 | 416.5 | 41.4 | 239 | 15 | US-10-148-953A-3 | Sequence 3, Appl1 |
| 25 | 415.5 | 41.3 | 152 | 14 | US-10-158-769-2 | Sequence 2, Appl1 |
| 26 | 414.5 | 41.2 | 233 | 16 | US-10-659-705-3 | Sequence 3, Appl1 |
| 27 | 413 | 41.0 | 236 | 13 | US-10-087-192-1953 | Sequence 1953, Ap |
| 28 | 412.5 | 41.0 | 239 | 15 | US-10-277-693A-10 | Sequence 10, Appl1 |
| 29 | 412.5 | 41.0 | 239 | 15 | US-10-003-632C-10 | Sequence 10, Appl1 |
| 30 | 412.5 | 41.0 | 239 | 15 | US-10-003-632C-13 | Sequence 13, Appl1 |
| 31 | 410.5 | 40.8 | 239 | 8 | US-08-726-211-5 | Sequence 5, Appl1 |
| 32 | 410.5 | 40.8 | 239 | 10 | US-09-993-420A-8 | Sequence 8, Appl1 |
| 33 | 410.5 | 40.8 | 239 | 14 | US-10-101-482-12 | Sequence 12, Appl1 |
| 34 | 410.5 | 40.8 | 239 | 14 | US-10-072-830-2 | Sequence 2, Appl1 |
| 35 | 410.5 | 40.8 | 239 | 14 | US-10-141-618-12 | Sequence 12, Appl1 |
| 36 | 410.5 | 40.8 | 239 | 14 | US-10-053-645A-21 | Sequence 21, Appl1 |
| 37 | 410.5 | 40.8 | 239 | 15 | US-10-387-961A-5 | Sequence 5, Appl1 |
| 38 | 410.5 | 40.8 | 239 | 15 | US-10-003-632C-1 | Sequence 1, Appl1 |
| 39 | 410.5 | 40.8 | 239 | 15 | US-10-003-632C-3 | Sequence 3, Appl1 |
| 40 | 410.5 | 40.8 | 239 | 15 | US-10-148-953A-1 | Sequence 1, Appl1 |
| 41 | 410.5 | 40.8 | 239 | 15 | US-10-148-953A-2 | Sequence 2, Appl1 |
| 42 | 410.5 | 40.8 | 239 | 15 | US-10-297-321-2 | Sequence 2, Appl1 |
| 43 | 410.5 | 40.8 | 239 | 16 | US-10-450-366-4 | Sequence 4, Appl1 |
| 44 | 410.5 | 40.8 | 239 | 16 | US-10-770-668-16 | Sequence 16, Appl1 |
| 45 | 410.5 | 40.8 | 485 | 16 | US-10-792-517-8 | Sequence 8, Appl1 |

ALIGNMENTS

RESULT 1
US-09-925-674A-7
Sequence 7, Application US/09925674A
Patent No. US20020119943A1
GENERAL INFORMATION:
APPLICANT: AMRAD Operations Pty Ltd
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
FILE REFERENCE: 11686A
CURRENT APPLICATION NUMBER: US/09/925,674A
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/925,674
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: P8965
PRIOR FILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentm Ver. 2.1
SEQ ID NO 7
LENGTH: 193
TYPE: PRT
ORGANISM: HUMAN
US-09-925-674A-7

Query Match 100.0%; Score 1007; DB 9; Length 193;
Beat Local Similarity 100.0%; Pred. No. 7.9e-97;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASPDRALVADPVGKLRQKGYVCAGPBGPAADPLHQAMRAGDEFETRRRT 60
Db 1 MATPASPDRALVADPVGKLRQKGYVCAGPBGPAADPLHQAMRAGDEFETRRRT 60
QY 61 FSDIAAGLHTTPGSAOQRFQVSDLEFGQGPMMGRLLVAFVFGAALCAESVNMKEPLVG 120
Db 61 FSDIAAGLHTTPGSAOQRFQVSDLEFGQGPMMGRLLVAFVFGAALCAESVNMKEPLVG 120
QY 121 QVQEMWVAIVETRLADWIHSSGGWAEFTALYGDGALBEARLRREGNMAVRYTLTGAVALL 180

Db 121 QOEWMMVAVLETRLDWTHSSGMAEFTALYGDALBEARLRREGNMAVTRVLTGAVAL 180
QY 181 GALVTGAFPFASK 193
Db 181 GALVTGAFPFASK 193

RESULT 2

US-10-450-366-6
; Sequence 6, Application US/10450366
; Publication No. US20040115667A1
; GENERAL INFORMATION:

APPLICANT: Tschopp, Jorg
APPLICANT: Hoffmann, Kay

TITLE OF INVENTION: DNA-Sequences, which Code for An Apoptosis Signal Transduction Pr
FILE REFERENCE: 11436*3

CURRENT APPLICATION NUMBER: US/10/450,366

PRIOR APPLICATION NUMBER: 2003-11-21

PRIOR FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: DE 100 61 766.2

PRIOR FILING DATE: 2000-12-12

PRIOR APPLICATION NUMBER: DE 101 00 280.7

PRIOR FILING DATE: 2001-01-04

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Version 3.1

SEQ ID NO 6

LENGTH: 193

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Human Bcl-w

US-10-450-366-6

Query Match

Best Local Similarity 100.0%; Score 1007; DB 16; Length 193;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60

Db 1 MATPASAPDTRALVADPFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60

QY 61 FSDLAQQLHVTGSAQOQFTQVSDLEFQGGPNMGRVAFVFGAALCAESVNMKEMEPLVG 120

Db 61 FSDLAQQLHVTGSAQOQFTQVSDLEFQGGPNMGRVAFVFGAALCAESVNMKEMEPLVG 120

QY 121 QOEWMMVAVLETRLDWTHSSGMAEFTALYGDALBEARLRREGNMAVTRVLTGAVAL 180

Db 121 QOEWMMVAVLETRLDWTHSSGMAEFTALYGDALBEARLRREGNMAVTRVLTGAVAL 180

QY 181 GALVTGAFPFASK 193

Db 181 GALVTGAFPFASK 193

RESULT 3

US-09-925-674A-9

; Sequence 9, Application US/09925674A

; Patent No. US20020119943A1

; GENERAL INFORMATION:

APPLICANT: AMRAD Operations Pty Ltd

TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2

FILE REFERENCE: 11686A

CURRENT APPLICATION NUMBER: US/09/925,674A

PRIOR FILING DATE: 2001-08-09

PRIOR APPLICATION NUMBER: P8965

PRIOR FILING DATE: 1996-03-27

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mouse
US-09-925-674A-9

Query Match 99.0%; Score 997; DB 9; Length 193;
Best Local Similarity 96.4%; Pred. No. 8,7e-96;

Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60

Db 1 MATPASAPDTRALVADPFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60

QY 61 FSDLAQQLHVTGSAQOQFTQVSDLEFQGGPNMGRVAFVFGAALCAESVNMKEMEPLVG 120

Db 61 FSDLAQQLHVTGSAQOQFTQVSDLEFQGGPNMGRVAFVFGAALCAESVNMKEMEPLVG 120

QY 121 QOEWMMVAVLETRLDWTHSSGMAEFTALYGDALBEARLRREGNMAVTRVLTGAVAL 180

Db 121 QOEWMMVAVLETRLDWTHSSGMAEFTALYGDALBEARLRREGNMAVTRVLTGAVAL 180

QY 181 GALVTGAFPFASK 193

Db 181 GALVTGAFPFASK 193

RESULT 4

US-09-809-391-696

; Sequence 696, Application US/09809391

; Publication No. US20030049618A1

; GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: P2002P2

CURRENT APPLICATION NUMBER: US/09/809,391

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 761

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 696

LENGTH: 365

TYPE: PRT

ORGANISM: Homo sapiens

US-09-809-391-696

Query Match

Best Local Similarity 76.1%; Score 766; DB 10; Length 365;

Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60

Db 1 MATPASAPDTRALVADPFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60

QY 61 FSDLAQQLHVTGSAQOQFTQVSDLEFQGGPNMGRVAFVFGAALCAESVNMKEMEPLVG 120

Db 61 FSDLAQQLHVTGSAQOQFTQVSDLEFQGGPNMGRVAFVFGAALCAESVNMKEMEPLVG 120

QY 121 QOEWMMVAVLETRLDWTHSSGMAEFTALYGDALBEARLRREGNMAVTRVLTGAVAL 180

Db 121 QOEWMMVAVLETRLDWTHSSGMAEFTALYGDALBEARLRREGNMAVTRVLTGAVAL 180

QY 181 GALVTGAFPFASK 193

Db 181 GALVTGAFPFASK 193

RESULT 5

US-09-882-171-696

; Sequence 696, Application US/09882171

; Publication No. US20030175858A1

; GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: P2002P2

CURRENT APPLICATION NUMBER: US/09/882,171

PRIOR FILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: 60/047,586
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,590
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,594
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,589
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,593
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,614
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043,578
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,576
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/047,501
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043,670
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/056,632
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,664
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,876
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,881
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,909
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,875
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,862
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,887
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,908
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/048,964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/057,650
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/057,669
PRIOR FILING DATE: 1997-09-05

Query Match 76.1%; Score 766; DB 10; Length 365;
Best Local Similarity 100.0%; Pred. No. 2,7e-71;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASADPTRALVADPVGYKLRQKGYCGAGPGEPAADPLHQMRAAGDEFETFRRT 60
DB 1 MATPASADPTRALVADPVGYKLRQKGYCGAGPGEPAADPLHQMRAAGDEFETFRRT 60
QY 61 FSDLAQLHTVTPGSAOORFTQVSDELFOGPNMGRIVAFVFGAALCAESVKNEMEPVVG 60
DB 61 FSDLAQLHTVTPGSAOORFTQVSDELFOGPNMGRIVAFVFGAALCAESVKNEMEPVVG 120
QY 121 QVQEMWVAVLETRLADWIHSSGWM 144
DB 121 QVQEMWVAVLETRLADWIHSSGWM 144

RESULT 6
US-10-164-861-696
Sequence 696, Application US/10164861
Publication No. US20030225248A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OR INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/10/164,861

CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 696
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
US-10-164-861-696

Query Match 76.1%; Score 766; DB 15; Length 365;
Best Local Similarity 100.0%; Pred. No. 2,7e-71;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASADPTRALVADPVGYKLRQKGYCGAGPGEPAADPLHQMRAAGDEFETFRRT 60
DB 1 MATPASADPTRALVADPVGYKLRQKGYCGAGPGEPAADPLHQMRAAGDEFETFRRT 60
QY 61 FSDLAQLHTVTPGSAOORFTQVSDELFOGPNMGRIVAFVFGAALCAESVKNEMEPVVG 120
DB 61 FSDLAQLHTVTPGSAOORFTQVSDELFOGPNMGRIVAFVFGAALCAESVKNEMEPVVG 120
QY 121 QVQEMWVAVLETRLADWIHSSGWM 144
DB 121 QVQEMWVAVLETRLADWIHSSGWM 144

RESULT 7
US-10-659-705-2
Sequence 2, Application US/10659705
Publication No. US20040117867A1
GENERAL INFORMATION:
APPLICANT: Look, A. Thomas
TITLE OR INVENTION: Transgenic Cancer Models in Fish
FILE REFERENCE: 112706.123
CURRENT FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US/10/659,705
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 228
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: BCL2 proteins
US-10-659-705-2

Query Match 62.3%; Score 627.5; DB 16; Length 228;
Best Local Similarity 66.8%; Pred. No. 4,4e-57;
Matches 123; Conservative 21; Mismatches 37; Indels 3; Gaps 1;

QY 10 TRALVADPVGYKLRQKGYCGAGPGEPAADPLHQMRAAGDEFETFRRTFSDLAQLH 69
DB 48 SRALVEDIVRYKLCQKSLV---PEPSGAASCALHSMRAAGDEFETFRROAFSISTQIH 104
QY 70 VTPGSAOORFTQVSDELFOGPNMGRIVAFVFGAALCAESVKNEMEPVVGQVQEMWVA 129
DB 105 VTPGSAOORFTQVSDELFOGPNMGRIVAFVFGAALCAESVKNEMEPVVGPRIDQWNVTV 164
QY 130 LETRLADWIHSSGWMFTALYGDGALAEARLRLEGNWASRYTLTGAVAGALVTVGAF 189
DB 165 LETRLADWIHSSGWMFTALYGDGALAEARLRLEGNWASRYTLTGAVAGALVTVGAF 224
QY 190 FASK 193
DB 225 FASK 228

RESULT 8
US-10-402-017-6
; Sequence 6, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 179
; TYPE: PRN
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del126-83)
US-10-402-017-6

Query Match 45.4%; Score 457.5; DB 15; Length 179;
Best Local Similarity 52.0%; Pred. No. 1.8e-39;
Matches 91; Conservative 21; Mismatches 56; Indels 7; Gaps 2;

QY 11 RALVADPFGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEPFRRTFSDLAQLAV 70
DB 6 RELVVDPLSYKLSQKGYVSWGAA-----AAAVKQALREAGDEFLRYRAAFSDLTSLHI 60

QY 71 TPGSAQGRFTQVSDLEFQGGPNNRGLVAFVFGAALCAESVKNKEMELVGVQVEMVAYL 130
DB 61 TPGTAQVQSFQVNVNELFRDGVNMGRIYAFPSFGALCVESVDKXMQVLRISAWMATYL 120

QY 131 EFTLADMIHSSGMAEFTALYGDGALREARLR--GNWASVRYVLGAVALLGL 183
DB 121 NDHLEPWIQDNGMDTFVELYGNNAAESRKQERFNRWFLTGMTVAGVLLGSL 175

RESULT 9
US-10-402-017-8
; Sequence 8, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 199
; TYPE: PRN
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del146-83)
US-10-402-017-8

Query Match 44.5%; Score 448.5; DB 15; Length 199;
Best Local Similarity 47.9%; Pred. No. 1.8e-38;
Matches 91; Conservative 21; Mismatches 61; Indels 17; Gaps 2;

QY 11 RALVADPFGYKLRQKGYV-----GAGPGEPAADPLHQAMRAAGDEFT 55
DB 6 RELVVDPLSYKLSQKGYVSWGQFSDVEENRTEAPEGTSESRAPAAAAYKQALREAGDEFL 65

QY 56 RFRRTFSDLAQLHVTGSAQGRFTQVSDLEFQGGPNNRGLVAFVFGAALCAESVKNEM 115

DB 66 RYRARFSDLTSLQHLIPGTAYQSFQGVNVELFRDGVNMGRIYAFPSFGALCVESVDKEM 125
QY 116 EPLVGVQVEMVAYLLETRLADMIHSSGMAEFTALYGDGALREARLR--GNWASRTV 173
DB 126 QVLVSRIASWMAATYLDHLEPWIQDNGMDTFVELYGNNAAESRKQERFNRWFLTGMT 185

QY 174 LTGAVALLGL 183
DB 186 VAGVLLGSL 195

RESULT 10
US-10-402-017-10
; Sequence 10, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 219
; TYPE: PRN
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del166-83)
US-10-402-017-10

Query Match 43.8%; Score 441.5; DB 15; Length 219;
Best Local Similarity 43.3%; Pred. No. 1.1e-37;
Matches 91; Conservative 21; Mismatches 61; Indels 37; Gaps 2;

QY 11 RALVADPFGYKLRQKGYV-----CGAGPGE 35
DB 6 RELVVDPLSYKLSQKGYVSWGQFSDVEENRTEAPEGTSESRTPSAINGNPSWMLADSPAV 65

QY 36 GPAADPLHQAMRAAGDEPFRRTFSDLAQLHVTGSAQGRFTQVSDLEFQGGPNNR 95
DB 66 AAAAAYKQALREAGDEFLRYRAAFSDLTSLQHLIPGTAYQSFQGVNVELFRDGVNMG 125

QY 96 LVAFVFGAALCAESVKNKEMELVGVQVEMVAYLLETRLADMIHSSGMAEFTALYGDGA 155
DB 126 IVAFPSFGALCVESVDKXMQVLSRIASWMAATYLDHLEPWIQDNGMDTFVELYGNNA 185

QY 156 LLEBARLR--GNWASVRYVLGAVALLGL 183
DB 186 AASRKQERFNRWFLTGMTVAGVLLGSL 215

RESULT 11
US-10-402-017-12
; Sequence 12, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 219

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del26-83)
US-10-402-017-12

Query Match 43.3%; Score 436.5; DB 15; Length 219;
Best Local Similarity 44.1%; Pred. No. 3.7e-37;
Matches 93; Conservative 22; Mismatches 57; Indels 39; Gaps 4;

11 RALVADPFGYKLRQGY-----VCGAGPEGPAAD-- 40
6 RELVDFLSYKLSQKGYSWSQSDVEENRTEAPEGTSEERRAAAVNGA-TGHSSSLDAR 64
41 -----PLHQAMRAAGDEFETFRRTFSDLAQLHTVTPGSAQORFTQVSDLFQGGPMWG 94
65 EVIPMAAVKQALRENGDEFELRYRAFSLTSLQHLTPGTATQSEQVYVNELFRGVNMG 124
95 RLVAFVFGALCAESVKNEMEPVGVQVQEMVAVYLETRLADWHSQGMAEFTALYGDG 154
125 RLVAFVFGALCVESVDKEMQVLVSRIASMTATYINDHLEPMIDNGMDTFVELYGN 184
155 ALERARLR--GNMASVTVLTGAVNAGAL 183
185 AAESRKGQERFRNRMFLGTMVAGVLLGSL 215

RESULT 12
US-10-792-517-2
Sequence 2, Application US/10792517
Publication No. US20040152179A1

GENERAL INFORMATION:
APPLICANT: Youle et al.
TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL
FILE REFERENCE: 4239-55417
CURRENT APPLICATION NUMBER: US/10/792,517
PRIOR FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/639,245
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/149,220
PRIOR FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: genetic fusion
US-10-792-517-2

Query Match 43.0%; Score 433.5; DB 16; Length 411;
Best Local Similarity 39.9%; Pred. No. 1.7e-36;
Matches 93; Conservative 26; Mismatches 63; Indels 51; Gaps 4;

11 RALVADPFGYKLRQGY-----VCGAGP-----GEGPAA 39
26 RELVDFLSYKLSQKGYSWSQSDVEENRTEAPEGTSEMETPSAINGNSWMLADSPAV 85
40 D-----PLHQAMRAAGDEFETFRRTFSDLAQLHTVTPGSAQORFTQ 81
86 NGATRAHSSLDARAVIPMAAVKQALRENGDEFELRYRAFSLTSLQHLTPGTATQSE 145
82 VSDLEFQGGPMWGLVAFVFGALCAESVKNEMEPVGVQVQEMVAVYLETRLADWHS 141
146 VVNELEFRDGVNMGRIVAFVFGALCVESVDKEMQVLVSRIASMTATYINDHLEPMI 205
142 GMAEFTALYGDGALERARLR--GNMASVTVLTGAVNAGALVTVGAFFAS 192
206 GGMDTFVELYGNMAAASRKGQERFRNRMFLGTMVAGVLLGSLFRKAVSAA 258

RESULT 13
US-10-659-705-7
Sequence 7, Application US/10659705
Publication No. US20040117867A1

GENERAL INFORMATION:
APPLICANT: Look, A. Thomas
TITLE OF INVENTION: Transgenic Cancer Models in Fish
FILE REFERENCE: 112706.123
CURRENT APPLICATION NUMBER: US/10/659,705
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 60/409,585
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 229
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: BCL2 proteins
US-10-659-705-7

Query Match 42.9%; Score 432.5; DB 16; Length 229;
Best Local Similarity 41.7%; Pred. No. 1e-36;
Matches 95; Conservative 22; Mismatches 62; Indels 49; Gaps 4;

11 RALVADPFGYKLRQGY-----VCGAGPEGP----- 37
6 RELVDFVSYKLSQKGYSELEEDENRTDPAALAMDSVLNGSPSWHPAGHYVNGAT 65
38 -----AADLHQAMRAAGDEFETFRRTFSDLAQLHTVTPGSAQORFTQVSD 85
66 VHSSLEHETVPAASVVRQALRDAGDEFELRYRAFSLTSLQHLTPGTATQSEQVNE 125
86 LFGGPMWGLVAFVFGALCAESVKNEMEPVGVQVQEMVAVYLETRLADWHSQGM 145
126 LFHDGVNMGRIVAFVFGALCVESVDKEMQVLVSRIASMTATYINDHLEPMI 185
146 EFTALYGDGALERARLR--GNMASVTVLTGAVNAGALVTVGAFFAS 193
186 RFVDLYGNNA--AAELRKGQETFMKMLTGTAVAGVLL-LGSLLSRK 229

RESULT 14
US-10-402-017-4

Sequence 4, Application US/10402017
Publication No. US20030219871A1
GENERAL INFORMATION:
APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENBERGER
TITLE OF INVENTION: Host cells having improved survival properties and methods to gene
FILE REFERENCE: Case 1/1314
CURRENT APPLICATION NUMBER: US/10/402,017
PRIOR FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: US 60/369,307
PRIOR APPLICATION NUMBER: April 2, 2002
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 233
TYPE: PRT
ORGANISM: Cricetus griseus

US-10-402-017-4

Query Match 42.7%; Score 429.5; DB 15; Length 233;
Best Local Similarity 41.3%; Pred. No. 2.2e-36;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

11 RALVADPFGYKLRQGY-----V----- 28
6 RELVDFLSYKLSQKGYSWSQSDVEENRTEAPEGTSEMETPSAINGNSWMLADSPAV 65

QY 29 CGAGPGGEPAD-----PLHQAMRAAGDEFETFRRTESDLAOLHTVPGSAOGRFT 80
 Db 66 NGA-TGHSSTSLDAREVTPMAAVKQALREAGDEFELRYRARSDDLTSQHLITPGTAYSQFE 124
 QY 81 QVSDLEFQGGPNMGRIVAFVFGAALCAESVKNEMEPVGVQOEWVAVYLETRLADWTHS 140
 Db 125 QVVELFRDGVNMGRIIVAFSFGALCVESVDKEMQVLSRIASMATYLNHDHLEPWIOD 184
 QY 141 SGGAAFTALYGDGALBEARLRE--GNMASVTVLTGAVALGAL 183
 Db 185 NGMDTFVELYGNNAAESRKQERFNRWFLTGMTVAGVLLGSL 229

RESULT 15

US-09-734-846-2
 ; Sequence 2, Application US/09734846
 ; Patent No. US20010007025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Dean, Nicholas M.
 ; APPLICANT: Morla, Brett P.
 ; APPLICANT: Nickoloff, Brian J.
 ; APPLICANT: Zhang, Qinqing
 ; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
 ; FILE REFERENCE: ISPH-0528
 ; CURRENT APPLICATION NUMBER: US/09/734,846
 ; PRIOR FILING DATE: 2000-12-12/09/277,020
 ; PRIOR APPLICATION NUMBER: 1998-03-26
 ; PRIOR FILING DATE: 1998-10-07/09/167,921
 ; PRIOR APPLICATION NUMBER: 1998-10-07
 ; PRIOR FILING DATE: 1999-06-02/09/323,743
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-734-846-2

Query Match 42.6%; Score 428.5; DB 9; Length 233;
 Best Local Similarity 40.6%; Pred. No. 2.8e-36;
 Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 PALVADVGYKLRQKY-----VCGAP---GEGPAA 39
 Db 6 RELVVDPLSYKLSQKGYSWQSPDVEENRTPEAGTSEMETPSAINGNPSMHLADSPAV 65
 QY 40 D-----PLHQAMRAAGDEFETFRRTESDLAOLHTVPGSAOGRFTQ 81
 Db 66 NGATNHSSTSLDAREVTPMAAVKQALREAGDEFELRYRARSDDLTSQHLITPGTAYSQFEQ 125
 QY 82 VSDLEFQGGPNMGRIVAFVFGAALCAESVKNEMEPVGVQOEWVAVYLETRLADWTHS 141
 Db 126 VVVELFRDGVNMGRIIVAFSFGALCVESVDKEMQVLSRIASMATYLNHDHLEPWIOD 185
 QY 142 SGGAAFTALYGDGALBEARLRE--GNMASVTVLTGAVALGAL 183
 Db 186 GGMDTFVELYGNNAAESRKQERFNRWFLTGMTVAGVLLGSL 229

Search completed: April 10, 2005, 22:59:27
 Job time: 228.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 10, 2005, 22:09:08 ; Search time 17 Seconds

(without alignments)
1092.343 Million cell updates/sec

Title: US-09-925-674B-7

Perfect score: 1007

Sequence: 1 MATPASAEDTRALVADPVG.....LTGAVLGLVTGAFPAASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 428.5 | 42.6 | 233 | 2 B47537 | apoptosis regulator |
| 2 | 428.5 | 42.6 | 233 | 2 I49056 | bcl-x long - mouse |
| 3 | 424.5 | 42.2 | 233 | 2 S51761 | Bcl-X protein - ra |
| 4 | 423.5 | 42.1 | 233 | 2 A37332 | transforming prote |
| 5 | 414 | 41.1 | 232 | 2 S24390 | transforming prote |
| 6 | 412.5 | 41.0 | 239 | 1 TVHUN1 | transforming prote |
| 7 | 412 | 40.9 | 236 | 2 I67432 | Bcl-2 - rat (fragm |
| 8 | 407 | 40.4 | 236 | 2 I53744 | gene bcl-2 protein |
| 9 | 406 | 40.3 | 236 | 1 TVMSA1 | transforming prote |
| 10 | 404.5 | 40.2 | 233 | 2 I67431 | Bcl-X-long - rat |
| 11 | 403 | 40.0 | 236 | 2 JC7383 | B-cell lymphoma 2 |
| 12 | 378 | 37.5 | 190 | 2 A47537 | apoptosis regulator |
| 13 | 377.5 | 37.5 | 214 | 2 I49057 | bcl-x transmembran |
| 14 | 375.5 | 37.3 | 227 | 2 JE0203 | apoptosis regulator |
| 15 | 356 | 35.4 | 216 | 2 B37332 | transforming prote |
| 16 | 349.5 | 34.7 | 199 | 1 TVMSB1 | transforming prote |
| 17 | 346 | 34.4 | 205 | 1 TVHUB1 | transforming prote |
| 18 | 277.5 | 27.6 | 154 | 2 I58194 | gene bcl-2 protein |
| 19 | 182 | 18.1 | 170 | 2 I49055 | bcl-x short - mouse |
| 20 | 176 | 17.5 | 211 | 2 S58873 | Bak protein - huma |
| 21 | 174 | 17.3 | 176 | 2 I67435 | gene bcl-xshort pr |
| 22 | 173 | 17.2 | 211 | 2 S58875 | cdn-2 protein - hu |
| 23 | 157.5 | 15.6 | 192 | 2 D47538 | bcl-2-associated p |
| 24 | 153 | 15.2 | 192 | 2 D47538 | bcl-2-associated p |
| 25 | 150 | 14.9 | 261 | 2 H88578 | protein ced-9 (imp |
| 26 | 150 | 14.9 | 261 | 2 A53189 | apoptosis suppress |
| 27 | 149.5 | 14.8 | 133 | 2 I53295 | bcl-2-associated p |
| 28 | 146.5 | 14.5 | 179 | 2 JC7255 | Bax-delta protein |
| 29 | 146.5 | 14.5 | 218 | 2 B47538 | bcl-2-associated p |

| | | | | | |
|----|-------|------|------|----------|----------------------|
| 30 | 143 | 14.2 | 177 | 2 S54778 | NR-13 protein - qu |
| 31 | 141 | 14.0 | 255 | 2 JC7567 | Mcl-1a protein - z |
| 32 | 137.5 | 13.7 | 143 | 2 I38921 | bcl-2-associated p |
| 33 | 118 | 11.7 | 175 | 2 I39055 | Bcl-2 related - hu |
| 34 | 112 | 11.1 | 350 | 2 A47476 | Bcl2 homolog MCL1 |
| 35 | 105 | 10.4 | 172 | 2 I49449 | hemopoietic-specific |
| 36 | 91.5 | 9.1 | 301 | 2 T36534 | probable lipase/es |
| 37 | 89 | 8.8 | 185 | 2 B83217 | hypothetical prote |
| 38 | 87 | 8.6 | 3433 | 1 GNMVTV | genome polypeptid |
| 39 | 85 | 8.4 | 270 | 2 A12558 | dihydrodipicolinat |
| 40 | 85 | 8.4 | 279 | 2 B97381 | dihydrodipicolinat |
| 41 | 84.5 | 8.4 | 358 | 1 AJLQCB | glutamate-ammonia |
| 42 | 83 | 8.2 | 417 | 2 T39939 | DNA binding protei |
| 43 | 82.5 | 8.2 | 1440 | 1 GNMVTF | genome polypeptid |
| 44 | 82.5 | 8.2 | 3432 | 1 GNMVTF | genome polypeptid |
| 45 | 81.5 | 8.1 | 354 | 2 S52040 | Gln 1.1 protein - |

ALIGNMENTS

```
RESULT 1
B47537
apoptosis regulator bcl-xl - human
N:Alternate names: bcl-2-related protein
N:Contains: apoptosis regulator bcl-xs
C:Species: Homo sapiens (man)
C:Accession: B47537
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A:Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A:Reference number: A47537; MUID:93364977; PMID:8358789
A:Accession: B47537
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <BOI>
A:Cross-references: UNIPROT:Q07817; GB:L20121; NID:G510900; PID:CAA80661.1; PID:G510901
A:Accession: C47537
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-69, 'G', '71-125, 189-233 <BO2>
A:Cross-references: GB:L20122; NID:G623236; PID:CAA80662.1; PID:G623237
C:Genetic:
A:Gene: GDB:BCL2L
A:Cross-references: GDB:228079
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: alternative splicing; apoptosis
F:1-233/Product: apoptosis regulator bcl-xl #status predicted <MAT>
F:1-125,189-233/Product: apoptosis regulator bcl-xs #status predicted <MA2>

Query Match 42.6%; Score 428.5; DB 2; Length 233;
Best Local Similarity 40.6%; Pred. No. 1.4e-37;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADPVGKYLKOKXV-----VCCAGP-----GEGPAA 39
DB 6 RELVDFLSYKLSQKXGWSQFSDVEENRTAEDEGTESENETPSALNGNSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFETFRFRRTSDLAQLHTPPGSAOQFTQ 81
DB 66 NGATTAHSSSLDAREVTPMAAVKQALREAGDEFELETRRAASDLSQHLTPGTAVQSFQ 125
QY 82 VSEDLQGGPNWGRVLAFFVGAALCAESVKNKMEPLVGQVQEMWVAYLETRLADWIHS 141
DB 126 VVNELEFDGVNMGRIYVFFSGGALCVESYDKEMQVLVSRIAAMWATYLLNDHLEPMIQEN 185
QY 142 GGAAEFTALYGDGALBEARLR--GNWASVRTVLGAVLGL 183
DB 186 GGDVTFVELYGNNAAESRKGQERFNRWFLTGKTVAGVLLGSL 229

RESULT 2
```

149056
 bcl-1 long - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: 149056; S52866
 R:Yang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
 J. Immunol. 153, 4388-4398, 1994
 A:Title: Cloning and molecular characterization of mouse bcl-1 in B and T lymphocytes.
 A:Reference number: 149055; MUID:95052604; PMID:7963517
 A:Accession: 149056
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-233 <RES>
 A:Cross-references: UNIPROT:Q64373; EMBL:U10101; NID:9506647; PID:AAA82173.1; PID:95066
 R:Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
 Submitted to the EMBL Data Library, November 1994
 A:Description: IL-5 inhibits anti-IGM-induced apoptosis in an immature B cell line throu
 A:Reference number: S52866
 A:Accession: S52866
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-233 <KAM>
 A:Cross-references: EMBL:X83574; NID:9695622; PID:CAA58557.1; PID:9695623
 C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.6%; Score 428.5; DB 2; Length 233;
 Best Local Similarity 41.3%; Pred. No. 1.4e-32;
 Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

11 PALVAFVGVYKLRQKGY-----V 28
 6 RELVDFLSYKLSQKGSWSQFSDVENRTPEETPEETPSAINGNPSMHLADSPAV 65
 29 CGAGPEGPAAD-----PLHQMRAAGDEFTFRFRFTSDLAQLHTVPGSAQORFT 80
 66 NGA-TGHSSTLDAREVITPMAAVKQALREAGDEFELRYRAFSDLTSQHLTPGTAYOSFE 124
 81 QVSDLEFQGGPWWGRVAFVFGAALCAESVKNEMEPVGVQVQEMVAVYLETRLADWTHS 140
 125 QVNVLEFRDGVWGRIVAFVFGAALCAESVKNEMEPVGVQVQEMVAVYLETRLADWTHS 140
 141 SGWNAEFTLYDGDALBEARRLRE--GNWASVRYTLTGAVVAGAL 183
 185 NGGMDTFVDLYGNNAABESRKGQERFNRWFLTGMTVAGVVLGSL 229

RESULT 3
 S51761
 BCL-X protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C:Accession: S51761; S51762
 R:Michaelidis, T.M.
 Submitted to the EMBL Data Library, November 1994
 A:Reference number: S51761
 A:Accession: S51761
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <MTC>
 A:Cross-references: UNIPROT:P53563; EMBL:X82537; NID:9607176; PID:CAA57886.1; PID:96071
 A:Experimental source: embryonic; brain
 A:Note: smaller form due to splicing
 C:Genetics:
 A:Insertions: 125/3
 C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.2%; Score 424.5; DB 2; Length 233;

Best Local Similarity 41.3%; Pred. No. 3.4e-32;
 Matches 92; Conservative 22; Mismatches 56; Indels 53; Gaps 4;
 13 LVADFVGVYKLRQKGY-----VCG 30
 8 LVDVFLSYKLSQKGSWSQFSDVENRTPEETPEETPSAINGNPSMHLADSPAVNG 67
 31 AGPEGPAAD-----PLHQMRAAGDEFTFRFRFTSDLAQLHTVPGSAQORFTOV 82
 68 A-TGHSSTLDAREVITPMAAVKQALREAGDEFELRYRAFSDLTSQHLTPGTAYOSFEQV 126
 83 SDELFGQGPWWGRVAFVFGAALCAESVKNEMEPVGVQVQEMVAVYLETRLADWTHSSG 142
 127 VNELEFRDGVWGRIVAFVFGAALCAESVKNEMEPVGVQVQEMVAVYLETRLADWTHSSG 186
 143 GWNAEFTLYDGDALBEARRLRE--GNWASVRYTLTGAVVAGAL 183
 187 GMDTFVDLYGNNAABESRKGQERFNRWFLTGMTVAGVVLGSL 229

RESULT 4
 A37332
 transforming protein (bcl-2-alpha) - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
 C:Accession: A37332; S35453
 R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari
 A:Reference number: A37332; MUID:92375724; PMID:1508712
 A:Accession: A37332
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-233 <EGU>
 A:Cross-references: UNIPROT:Q00709; EMBL:D11381
 C:Genetics:
 A:Insertions: 189/3
 C:Superfamily: bcl apoptosis regulator, inhibitory type
 C:Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 42.1%; Score 423.5; DB 2; Length 233;
 Best Local Similarity 38.0%; Pred. No. 4.2e-32;
 Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;

9 DTRLVADFVGVYKLRQKGYVCGAG-----PGGPAADP----- 41
 10 DNREITLVRYHYKLSQNGYDWAAGEDRPVPAPAPAAVAAGASSHHRPEPPGSA 69
 42 -----LHQMRAAGDEFTFRFRFTSDLAQLHTVPGSAQORFTOVSD 84
 70 AASEVPAPAGURPAPPGVHIALRQAGDFSRRTYQDRFQMSGQHLTPFTHAGRFVAVVE 129
 85 ELFGQGPWWGRVAFVFGAALCAESVKNEMEPVGVQVQEMVAVYLETRLADWTHSSGW 144
 130 ELFRDGVWGRIVAFVFGAALCAESVKNEMEPVGVQVQEMVAVYLETRLADWTHSSGW 189
 145 AEFTLYDGDALBEARRLREGNWSVRYTLTGAVVAGVAVGAFRASK 193
 190 DAFVEIYGN-----SMRPLFDSWISLTKTILS-LVLVGACTTGAYVGHK 233

RESULT 5
 S24390
 transforming protein (bcl-2) homolog - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S24390
 R:Caizals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
 Biochim. Biophys. Acta 1132, 109-113, 1992
 A:Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue
 A:Reference number: S24390; MUID:92379084; PMID:1511008
 A:Accession: S24390
 A:Status: preliminary

A: Accession: A27622
A: Molecule type: mRNA

Db 1.90 GGWDAFVELYG---PSMRPLFDFSWQSLKTLISLAL-VGACITLGAYLGHK 236

Db 1.90 GGWDAFVELYG---PSMRPLFDFSWQSLKTLISLAL-VGACITLGAYLGHK 236

C/Genetics:
A:Gene: bcl-2
C:Superfamily: bcl apoptosis regulator, inhibitory type
C/Keywords: B-cell lymphoma; ovary

Query Match 40.0%; Score 403; DB 2; Length 236;
Best Local Similarity 35.3%; Pred. No. 3.5e-30;
Matches 82; Conservative 34; Mismatches 64; Indels 52; Gaps 3;

9 DTRALVADPVGYKLRQKGY-----
10 DNREIVKMYIHYKLSQSGYEMVDVDAAPLGAAPTFGIFSGQESNPTPAVHRDMAART 69
28 -----VCGAGPGSGPADPLHQAMRAAGDEFETFRRTFSDDLAAQLHTVPGSAOQRTQ 81
70 SPLRPVATGTPTLSPVPVVAHLTLRRAGDDFSRRYRDRDFAMSSQLHTPTFARGRAT 129
82 VSDLEFQGGPNMGRVAFVFGAALCAESVKNKEMEPVQGVQVEMVAVYLETPLADWISS 141
130 VVELFPRDGVNMGRIYVAFERFGVCMCVSVREMSPLVDNIALMTETLNLHITWIODN 189
142 GMAEFPTALYGDGALBEARLRLEGNNMVASRTVLTGAVAGALVTGVAEFPAK 193
190 GMDAFVETLYG-----PSVRPLDFDSWLSLTKTILSLAL-VGACITLTGYLGHK 236

RESULT 12

A47537
apoptosis regulator bcl-x - chicken
C/Species: Gallus gallus (chicken)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: A47537
R/Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74; 597-608, 1993.
A/Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptosis
A/Reference number: A47537; MUID:93364977; PMID:8358789
A/Accession: A47537
A:Status: preliminary
A:Molecule type: DNA
A/Residues: 1-190 <BOI>
A/Cross-references: UNIPROT:Q07816; GB:223110; GB:L20120; NID:9510898; PIDN:CAA80657.1;
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.5%; Score 378; DB 2; Length 190;
Best Local Similarity 43.8%; Pred. No. 5.9e-28;
Matches 81; Conservative 14; Mismatches 44; Indels 46; Gaps 3;

11 RALVADPVGYKLRQKGY-----VCGAGPGSGP-----
6 RELVIDVSYKLSQSGHWSLEBEDENRTTAAEEMDSVLNPSMHPAGHVNAGAT 65
38 -----AADPLHQAMRAAGDEFETFRRTFSDDLAAQLHTVPGSAOQRTQVSD 85
66 VHRSLFVHEIVRASDVQRALRDAGDEFELKRYRAFSDLTSQLHTPTAVQSFQVYVNE 125
86 LFOGPNMGRVAFVFGAALCAESVKNKEMEPVQGVQVEMVAVYLETPLADWISSGMA 145
126 LFHGVNMGRIYVAFERFGALCVESVDKEMQLVGRIVSMWTYLTDLHLEWQENGWV 185
146 EFTAL 150
186 R-TAL 189

RESULT 13

149057
bcl-x transmembrane deleted - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 149057
R/Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A/Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.

A/Reference number: 149055; MUID:95052604; PMID:7963517
A/Accession: 149057
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A/Residues: 1-214 <RES>
A/Cross-references: UNIPROT:Q64373; EMBL:U10102; NID:9506649; PIDN:AAA82174.1; PID:950664;

C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.5%; Score 377.5; DB 2; Length 214;
Best Local Similarity 42.8%; Pred. No. 7.6e-28;
Matches 80; Conservative 16; Mismatches 40; Indels 51; Gaps 3;

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6 RELVVDLSYKLSQKGSWSQPSDVEENRTTEAPETAEETPSAINGNPSWHLADSPAV 65
29 CGAGPGSGPAD-----PLHQAMRAAGDEFETFRRTFSDDLAAQLHTVPGSAOQRT 80
66 NGA-TGHSSSLDAREVTPMAAVKQALREAGDEFELKRYRAFSDLTSQLHTPTGTAYSFE 124
81 QVSDLEFQGGPNMGRVAFVFGAALCAESVKNKEMEPVQGVQVEMVAVYLETPLADWISS 140
125 QVNVLEFPRDGVNMGRIYVAFERFGALCVESVDKEMQVLGRIVSMWTYLTDLHLEWQ 184
141 SGGWAEF 147
185 NGGWDTF 191

RESULT 14

JE0203
apoptosis regulator bcl-x isoform - human
N/Alternate names: h-bcl-xbeta
C/Species: Homo sapiens (man)
C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C/Accession: JE0203
R/Ban, U.; Eckhart, L.; Weninger, W.; Mildner, M.; Techachler, B.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A/Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A/Reference number: JE0203; MUID:98340865; PMID:9675101
A/Accession: JE0203
A:Molecule type: mRNA
A/Residues: 1-227 <BAN>
A/Cross-references: UNIPROT:Q07817; GB:U72398; NID:91622940; PIDN:AA17354.1; PID:9162294;
C/Genetics:
A:Gene: bcl-x
A:Map position: 20
C:Superfamily: bcl apoptosis regulator, inhibitory type

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Matches 82; Conservative 18; Mismatches 50; Indels 51; Gaps 3;

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66 NGA-TGHSSSLDAREVTPMAAVKQALREAGDEFELKRYRAFSDLTSQLHTPTGTAYSFE 124
81 QVSDLEFQGGPNMGRVAFVFGAALCAESVKNKEMEPVQGVQVEMVAVYLETPLADWISS 140
125 QVNVLEFPRDGVNMGRIYVAFERFGALCVESVDKEMQVLGRIVSMWTYLTDLHLEWQ 184
141 SGGWAEFTALYGDGALBEAR 161
185 NGGWRTKPLVCPSPSLASGR 205

RESULT 15

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 14:45:43 ; Search time 3057.74 Seconds
(without alignments)
9206.966 Million cell updates/sec

Title: US-09-925-674B-8

Perfect score: 581
Sequence: 1 atgcgcagcccccagccctaac.....gccttttctgtagcaagtg 581

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: 1: gb_ba: 2: gb_hgt: 3: gb_in: 4: gb_cm: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_dl: 9: gb_pt: 10: gb_ro: 11: gb_str: 12: gb_sy: 13: gb_un: 14: gb_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 581 | 100.0 | 581 | 6 AX022531 | AX022531 Sequence |
| 2 | 581 | 100.0 | 581 | 6 AX030819 | AX030819 Sequence |
| 3 | 560.2 | 96.4 | 582 | 10 MM059746 | US9746 Mus musculu |
| 4 | 560.2 | 96.4 | 582 | 10 AF030769 | AF030769 Mus muscu |
| 5 | 549.2 | 94.5 | 3442 | 10 AK172925 | AK172925 Mus muscu |
| 6 | 544.2 | 93.7 | 582 | 10 AF096291 | AF096291 Rattus no |
| 7 | 544.2 | 93.7 | 1110 | 10 AY185100 | AY185100 Rattus no |
| 8 | 544.2 | 93.7 | 3487 | 10 AY185098 | AY185098 Rattus no |
| 9 | 544.2 | 93.7 | 3545 | 10 BC074021 | BC074021 Rattus no |
| 10 | 541 | 93.1 | 3473 | 10 AY170344 | AY170344 Mus muscu |
| 11 | 540.6 | 93.0 | 579 | 6 AR020779 | AR020779 Sequence |
| 12 | 505.8 | 87.1 | 582 | 6 AX481423 | AX481423 Sequence |
| 13 | 505.8 | 87.1 | 582 | 9 HSU59747 | HSU59747 Sequence |
| 14 | 502.6 | 86.5 | 3542 | 9 DB87461 | DB87461 Homo sapien |
| 15 | 501 | 86.2 | 582 | 6 CG730429 | CG730429 Sequence |
| 16 | 501 | 86.2 | 583 | 6 AX022529 | AX022529 Sequence |
| 17 | 497.4 | 85.6 | 579 | 6 AR020780 | AR020780 Sequence |
| 18 | 497.4 | 85.6 | 579 | 6 AR020780 | AR020780 Sequence |
| 19 | 451.4 | 77.7 | 220818 | 2 AC128940 | AC128940 Rattus no |

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| 20 | 451.4 | 77.7 | 223933 | 2 AC097389 | AC097389 Rattus no |
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| 24 | 407.4 | 70.1 | 263901 | 2 AC115371 | AC115371 Rattus no |
| 25 | 390.8 | 67.3 | 148278 | 2 AC079885 | AC079885 Rattus no |
| 26 | 390.8 | 67.3 | 180665 | 2 AC084240 | AC084240 Rattus no |
| 27 | 390.8 | 67.3 | 221557 | 2 AC134055 | AC134055 Rattus no |
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| 30 | 364.4 | 62.7 | 1864 | 6 BD191165 | BD191165 186 human |
| 31 | 364.4 | 62.7 | 1864 | 6 AX924675 | AX924675 Sequence |
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| 34 | 233.8 | 40.2 | 749 | 5 XLR1 | XLR1 X. laevis R1 |
| 35 | 232.6 | 40.0 | 1053 | 5 BC073259 | BC073259 Xenopus l |
| 36 | 232.6 | 40.0 | 1894 | 5 BC084445 | BC084445 Xenopus l |
| 37 | 212.2 | 36.5 | 6049 | 6 AX345130 | AX345130 Sequence |
| 38 | 191 | 32.9 | 6049 | 6 AX345131 | AX345131 Sequence |
| 39 | 142.4 | 24.5 | 1252 | 4 AB073983 | AB073983 Canis fam |
| 40 | 140.8 | 24.2 | 1163 | 4 AB080951 | AB080951 Felis cat |
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| 43 | 139.4 | 24.0 | 600 | 6 AX925692 | AX925692 Sequence |
| 44 | 139.2 | 24.0 | 702 | 4 AY005131 | AY005131 Oryctolag |
| 45 | 138.2 | 23.8 | 1184 | 5 GGU26645 | GGU26645 Gallus gall |

ALIGNMENTS

| | | | | | | |
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| LOCUS | AX022531 | | | | | |
| DEFINITION | Sequence 8 from Patent EP0932674. | | | | | |
| ACCESSION | AX022531 | | | | | |
| VERSION | AX022531.1 | GI:10046127 | | | | |
| KEYWORDS | | | | | | |
| SOURCE | unidentified | | | | | |
| ORGANISM | unclassified. | | | | | |
| REFERENCE | 1 | Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M. | | | | |
| AUTHORS | | A novel mammalian gene, bcl-2, belongs to the bcl-2 family of | | | | |
| TITLE | | apoptosis-controlling genes | | | | |
| JOURNAL | | Patent: EP 0932674-A 8 04-AUG-1999; | | | | |
| FEATURES | | AMRAD OPERATIONS PTY LTD (AU) | | | | |
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| | | AMRAAGDEFETRRRTTSIDLAQLHTVPSAQQRTQVSELTQGGFNWRILVAFVF | | | | |
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| ORIGIN | | | | | | |
| Query Match | | 100.0%; Score 581; DB 6; Length 581; | | | | |
| Best Local Similarity | | 100.0%; Pred. No. 9.9e-126; | | | | |
| Matches | | 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | |
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| DB | | 1 ATGCGGAGCCGAGCTCAACCCAGACAGCGGCTAGTGGCTGTTGGGTAT 60 | | | | |
| QY | | 61 AGGCTGAGGAGGAGGCTTATGCTGTGAGCTGGGCTGGGAGGCCAGCCGCGAC 120 | | | | |

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Db 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTG 581

RESULT 2
LOCUS AX030819 581 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 8 from Patent WO9735971.
ACCESSION AX030819
VERSION AX030819.1 GI:10278313
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.
AUTHORS A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
TITLE apoptosis-controlling genes
JOURNAL Patent: WO 9735971-A 8 02-OCT-1997;
ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAWN P (AU) ; CORY SUZANNE (AU)
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
FEATURES
SOURCE Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9, 9e-126;
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RESULT 3
LOCUS MMU59746 582 bp mRNA linear ROD 29-SEP-1996
DEFINITION Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION U59746
VERSION U59746.1 GI:1572494
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 582)
TITLE Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,
Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.,
JOURNAL bcl-w, a novel member of the bcl-2 family, promotes cell survival
MEDLINE Oncogene 13 (4), 665-675 (1996)
PUBMED 96358615
8761287

REFERENCE 2 (bases 1 to 582)
Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
Cory, S.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
Eliza Hall Institute of Medical Research, PO Royal Melbourne
Hosptal, Parkville, Victoria 3050, Australia
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SOURCE Location/Qualifiers
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CDS

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ORIGIN

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Query Match      96.4%; Score 560.2; DB 10; Length 582;
Best Local Similarity 97.8%; Pred. No. 7.5e-121;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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RESULT 4

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DEFINITION Mus musculus BCL-W (Bcl-w) mRNA, complete cds.
ACCESSION AF030769
VERSION AF030769.1 GI:2623249
KEYWORDS
SOURCE

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ORGANISM

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Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3476)
Roos,A.J., Waymire,K.G., Moss,J.E., Parlow,A.F., Russell,L.D. and
Macgregor,G.R.

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TITLE

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Bcl-w is required for testis homeostasis
2 (bases 1 to 3476)
Roos,A.J. and Macgregor,G.R.
Direct Submission
Submitted (21-OCT-1997) Center for Molecular Medicine, Emory
University, 1462 Clifton Road, Atlanta, GA 30322, USA

FEATURES

SOURCE

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/mol_type="mRNA"

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83. 170

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179. 760

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611. 3476

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/number=4

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/note="mRNA destabilization element"

3428. 3441

/gene="Bcl-w"

ORIGIN

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Query Match      96.4%; Score 560.2; DB 10; Length 3476;
Best Local Similarity 97.8%; Pred. No. 5.6e-121;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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 ACCESSION AKI72925
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 TITLE Okazaki, N., Kikuno, R.F., Ohara, R., Inamoto, S., Koseki, H., Kiyooka, S., Suga, Y., Saito, S., Nishimura, H., Ohara, O. and Koga, H., Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries
 REFERENCE DNA Res. 11, 205-218 (2004)
 AUTHORS Okazaki, N., Kikuno, R.F., Ohara, R., Ohara, O. and Koga, H.
 JOURNAL Direct Submission
 COMMENT Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics, 2-6-7, Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918) The CREATE program supported by Japan science and technology corporation; cDNA full insert sequencing; Kazusa DNA Research Institute; cDNA library construction, clone selection and 5'- & 3'-end one pass sequencing.
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 ACCESSION AF096291
 VERSION AF096291.1 GI:3747129
 KEYWORDS SOURCE
 ORGANISM Rattus norvegicus (Norway rat)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
 TITLE Hamner, S., Skoglosa, Y. and Lindholm, D. Differential expression of bcl-w and bcl-x messenger RNA in the developing and adult rat nervous system
 REFERENCE Neurosci. 91 (2), 673-684 (1999)
 JOURNAL Hamner, S., Skoglosa, Y. and Lindholm, D. Direct Submission
 AUTHORS Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala University, Box 587, BMC, Uppsala 751 23, Sweden
 JOURNAL
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CDS

ORIGIN

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|------------------------|-------|-------------|
| Best Local Match | 93.7% | Score 544.2 |
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| Matches 558; Conserved | | |

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REFERENCE
AUTHORS
Stratton, I. to ...
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Worley, K.C., Malek, S., Loquelliano, N.A., Peters, G.I., Villalón, D.K., Hale, S., Gunaratne, P.H., McEwan, P.I., Fahney, J., Muzny, A., Garcia, A., Toshiyuki, S.

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1. J. A. Jones, S. S. J. Skalska, U. Smailus, D. E. Myers, R. M. Proctor, and initial analysis of more than 15
2. 12477932. Acad. Sci. U.S.A.

1999, 2000 full-length
sequences (26), 16899-16903 (2002)

Genome Collection (MGC), National Institute of Cancer, 31 Center, USA

NIH-MGC Project URL: <http://mgc.nhlbi.nih.gov>
 Contact: MGC help desk: mgc_help@nih.gov
 Email: mgc_help@nih.gov

CDNA Library Preparation: Howard Jacobson
Tissue Procurement: nih.gov
c9abds-remail.nih.gov

Genetically Arrayed by: Express Genomics
Sequencing by: The I.M.A.G.E. Consortium
Walthersburg (NISC) Institute

...ates of Health Intramural
...eolium (LNI)
...g, Maryland;
...ed site: <http://www.nisc.nih.gov/>
Contact: nisc_mg@hqr1.nih.gov/

406 UTM 5-5

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLM at: <http://image.llnl.gov>
 Series: IRAX Plate: 175 Row: P Column: 4
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AY170344

LOCUS

AY170344 Mus musculus Bcl2-like protein 2 mRNA, complete cds.

DEFINITION

AY170344

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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DEFINITION Sequence 1 from patent US 5789201.
ACCESSION AR020779
VERSION AR020779.1 GI:3975394
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 579)
AUTHORS Guastella, J.
TITLE Genes coding for bcl-2 and bcl-2 homologue
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Location/Qualifiers
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ORIGIN

Query Match 93.0%; Score 540.6; DB 6; Length 579;
Best Local Similarity 95.9%; Pred. No. 3e-116;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
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DEFINITION Sequence 37 from Patent WO02055693.
ACCESSION AX481423
VERSION AX481423.1 GI:22316337
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kreutzler, R., Limer, S., Roat, S., and Hadjiger, P.
TITLE Method for inhibiting the expression of a target gene
JOURNAL Patent: WO 02055693-A 37 18-JUL-2002;
FEATURES
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ORIGIN

Query Match 87.1%; Score 505.8; DB 6; Length 582;
Best Local Similarity 91.9%; Pred. No. 4.3e-108;
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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 LOCUS HSUS9747 582 bp mRNA linear PRI 29-SEP-1996
 DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.
 ACCESSION U59747
 VERSION U59747.1 GI:1572492
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS 1 (bases 1 to 582)
 Gjbson,L., Holmgren,S.P., Huang,D.C., Bernard,O., Copeland,N.G., Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S. bcl-w, a novel member of the bcl-2 family, promotes cell survival Oncogene 13 (4), 665-675 (1996)
 TITLE JOURNAL MEDLINE PUBMED
 8761287
 2 (bases 1 to 582)
 Gjbson,L., Holmgren,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and Cory,S. Direct Submission Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
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 Best Local Similarity 91.9%; Pred. No. 4.3e-108;
 Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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 DB 541 GGGGCGCTGGTAACTGTAGGGGCGCTTTTGTCTAGCAAGT 581
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 LOCUS DB87461 3542 bp mRNA linear PRI 10-JAN-2004
 DEFINITION Homo sapiens mRNA for KIAA0201 gene, partial cds.
 ACCESSION DB87461
 VERSION DB87461.1 GI:1944417
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS 1
 Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawabayashi,Y., Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N. Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
 JOURNAL MEDLINE PUBMED
 97191544
 2 (bases 1 to 3542)
 Nagase,T., Kikuno,R. and Nomura,N. Direct Submission Submitted (27-JUN-1996) Osamu Ohara, Kazuo DNA Research Institute; 1532-3, Yama, Kigazaki, Chiba 292-0812, Japan (E-mail:cdnainfo@kazuo.or.jp, Tel:+81-438-52-3913)
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ORIGIN

Query Match 86.5%; Score 502.6; DB 9; Length 3542;
Best Local Similarity 91.6%; Pred. No. 1.8e-107;
Matches 532; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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DB 177 ATGGAGACCCCAAGCTCTCGGCCCCAGACACACGCGCTGCTGTGACAGACTTTGTAGGCTAT 236
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LOCUS CO730429 582 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 16363 from Patent WO02068579.
ACCESSION CO730429
VERSION CO730429.1 GI:42304244
KEYWORDS
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.

TITLE

Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof.

JOURNAL

Patent: WO 02068579-A 16363 06-SEP-2002;

FEATURES

PE Corporation (NY) (US)
Location/Qualifiers
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/organism="Homo sapiens"
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source

ORIGIN

Query Match 86.2%; Score 501; DB 6; Length 582;
Best Local Similarity 91.4%; Pred. No. 5.8e-107;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Search completed: April 10, 2005, 18:37:59
Job time : 3063.74 secs

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| 26 | 212.2 | 36.5 | 6049 | 6 | ABL32228 | Ab132228 | Human | imm | |
| 27 | 191 | 32.9 | 6049 | 6 | ABL32229 | Ab132229 | Human | imm | |
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| 29 | 139.6 | 24.0 | 540 | 12 | ADH52634 | Adh52634 | Chinese | h | |
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| 31 | 138.8 | 23.9 | 151 | 12 | ACH93889 | Ach93889 | Human | gen | |
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| 36 | 137.8 | 23.7 | 150 | 4 | ABA47382 | Abas47382 | Human | bre | |
| 37 | 137.8 | 23.7 | 150 | 4 | ABA33370 | Abas33370 | Probe | #10 | |
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ALIGNMENTS

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| XX | |
| DT | 22-APR-1998 (first entry) |
| XX | |
| DE | Mouse bcl-w DNA. |
| XX | |
| KW | Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; |
| KW | diagnosis; degenerative disease; ss. |
| XX | |
| OS | Mus sp. |
| XX | |
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| FT | /product= "bcl-w" |
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| XX | |
| PN | W09735971-A1. |
| XX | |
| PD | 02-OCT-1997. |
| XX | |
| PF | 27-MAR-1997; 97MO-AU000199. |
| XX | |
| PR | 27-MAR-1996; 96AU-00008965. |
| XX | |
| PA | (AMRA-) AMRAD OPERATIONS PTY LTD. |
| XX | |
| PI | Cory S, Adams JM, Gibson LM, Holmgreen SP; |
| XX | |
| DR | WPI; 1997-489635/45. |
| DR | P-PSDB; AAM36048. |
| XX | |
| PT | Nucleic acid encoding apoptosis related gene bcl-w - used to induce or |
| PT | inhibit cell survival, e.g. for treatment of cancer and degenerative |
| XX | diseases. |
| XX | |
| PS | Claim 3; Page 50-51; 86pp; English. |
| XX | |
| CC | This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene |

CC family. This gene promotes cell survival, so its modulation is useful in
 CC treatment of cancer or auto-immune diseases, degenerative diseases (e.g.
 CC stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,
 CC hypoxia, ischemia, human immunodeficiency virus infection or in cell
 CC transplants. Up-regulation of the gene can also be used to modify cell
 CC lines cultured in vivo, e.g. to develop new lines, to facilitate
 CC isolation of hybridomas and to increase survival of primary cell
 CC during genetic modification. It can be used to produce recombinant Bcl-w
 CC for therapy, diagnosis, antibody production or screening of potential
 CC modulators
 XX
 CC

Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0 Other;
 Query Match 100.0%; Score 581; DB 2; Length 581;
 Best Local Similarity 100.0%; Pred. No. 8.4e-148;
 Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCACTTCAACCCCAAGCAGCCCTCTAGTGGCTGACTTTGAGGCTAT 60
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 QY 541 GGGGCGCTGTGTAAGTGTAGGGGCTTTTCTTGAAGAGT 581
 DB 541 GGGGCGCTGTGTAAGTGTAGGGGCTTTTCTTGAAGAGT 581

RESULT 2
 AAX25135
 ID AAX25135 standard; DNA; 581 BP.
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 AC AAX25135;
 XX
 DT 05-JUL-1999 (first entry)
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 DE Mouse bcl-w gene derivative.
 XX
 KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
 XX animal model; ss.
 XX
 OS Mus sp.

EH Key Location/Qualifiers
 FT CDS 1..507
 FT CDS /*tag= a
 PN MO9913710-AL
 PD 25-MAR-1999.
 PF 16-SEP-1998; 98MO-AU000764.
 PF 16-SEP-1997; 97AU-00009228.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 DR WPI: 1999-243890/20.
 DR P-PSDB; AA05533.
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 PS Disclosure; Page 38; 52pp; English.

CC The present sequence is described as a derivative of the mouse bcl-w gene
 CC (see AAX25133) and encodes Bcl-w protein (see AA05533), a pro-survival
 CC member of the Bcl-2 family which is widely expressed and which is a
 CC essential for spermatogenesis. The invention relates generally to a
 CC method of treatment and to an animal model for the identification of
 CC molecules and genetic sequences useful for inducing or reducing fertility
 CC or for reducing fertility, by modulating spermatogenesis. An animal model
 CC carries a mutation is at least one allele of the human or murine bcl-w
 CC gene or in a gene associated with bcl-w. Such animals have disorganized
 CC seminiferous tubules and are substantially infertile, but possess no other
 CC major abnormalities as determined by histological examination. They can
 CC be used to screen for therapeutic molecules including genetic. They can
 CC be capable of inducing, enhancing or otherwise facilitating spermatogenesis
 CC in animals, or which can induce infertility

Query Match 100.0%; Score 581; DB 2; Length 581;
 Best Local Similarity 100.0%; Pred. No. 8.4e-148;
 Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCACTTCAACCCCAAGCAGCCCTCTAGTGGCTGACTTTGAGGCTAT 60
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 QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGAGAGTTGAGACCCGTTTCGCGACAC 120
 DB 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGAGAGTTGAGACCCGTTTCGCGACAC 120
 QY 181 TTCTGTACCTGGCCGCTGAGTCAACAGTGAACCCCAAGCTCAAGCCGTTTCGCGACAC 180
 DB 181 TTCTGTACCTGGCCGCTGAGTCAACAGTGAACCCCAAGCTCAAGCCGTTTCGCGACAC 180
 QY 241 CAGGTTTCGACGCACTTTTCCAAAGGGGCGCTTAACTGGGCGCTTGTGGCAATCTTT 240
 DB 241 CAGGTTTCGACGCACTTTTCCAAAGGGGCGCTTAACTGGGCGCTTGTGGCAATCTTT 240
 QY 301 GTCCTTGGGGGCTGCTGCTGTGCTGAGAGTGTCAAAAGAAATGAGAGCTTTGGTGGGA 300
 DB 301 GTCCTTGGGGGCTGCTGCTGTGCTGAGAGTGTCAAAAGAAATGAGAGCTTTGGTGGGA 300
 QY 361 CAAGTCCAGAGATTGATGCTGGGCTTACCTGAGACAGCTGTGGCTGAGATCCACAGC 420
 DB 361 CAAGTCCAGAGATTGATGCTGGGCTTACCTGAGACAGCTGTGGCTGAGATCCACAGC 420

1 ATGCCGACCCAGCCTCAACCCAGACACACGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

PR 08-MAY-2002; 2002US-0378370P.
PR 08-MAY-2002; 2002US-0378653P

PR 09-MAY-2002; 2002US-0378653P.
 PR 09-MAY-2002; 2002US-0378655P.
 PR 09-JUL-2002; 2002US-0394230P.
 PR 09-JUL-2002; 2002US-0394253P.
 PR 04-SEP-2002; 2002US-0407688P.
 PR 28-JAN-2003; 2003US-0442900P.

(GENE-) GENE LOGIC INC.

PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M,
 PI Elashoff M;
 DR MPI; 2003-731472/69.

XX Determining if a compound induces a toxic effect on a tissue or cell, for
 PT identifying hepatotoxic compounds, comprises comparing a gene expression
 PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
 XX mean values.

PS Claim 44; SEQ ID NO 3538; 874bp; English.

XX The present invention describes a method for determining whether a
 CC compound induces a toxic effect on a tissue or cell. The method comprises
 CC preparing a gene expression profile of a tissue or cell sample exposed to
 CC the compound, and comparing the gene expression profile to a database
 CC comprising data or information on the Tox mean and non-Tox mean value.
 CC The method is useful for predicting or identifying at least one toxic
 CC genes listed in the specification are useful as diagnostic or toxicity
 CC markers for the prediction or identification of the physiological state
 CC of tissue or cell sample that has been exposed to a compound or to
 CC identify or predict the toxic effects of a compound or an agent. These
 CC may also be used as markers for monitoring toxicity progression or for
 CC drug screening. The present sequence represents a primary rat hepatocyte
 CC toxicity modelling related gene sequence from the present invention.

SO Sequence 582 BP; 111 A; 157 C; 200 G; 114 T; 0 U; 0 Other;

Query Match 93.7%; Score 544.2; DB 10; Length 582;
 Best Local Similarity 96.0%; Pred. No. 8.5e-138;

Matches 558; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 ATGCGAAGCCGACCTCAACCCAGACACACGCGCTCTGAGTGGCTGACTTTGAGGCTAT 60
 DB 1 ATGCGAAGCCGACCTCAACCCAGACACACGCGCTCTGAGTGGCTGACTTTGAGGCTAT 60
 QY 61 AGGCTGAGGACGAGAGGATTATGCTGTGAGAGCTGGGCTGGGAGAGCCGACCGGAC 60
 DB 61 AGGCTGAGGACGAGAGGATTATGCTGTGAGAGCTGGGCTGGGAGAGCCGACCGGAC 60
 QY 121 CCGCTGACACAGGCAATGCGGCTCTGAGAGACGATTGAGACCGCTTCCGCGAC 120
 DB 121 CCGCTGACACAGGCAATGCGGCTCTGAGAGACGATTGAGACCGCTTCCGCGAC 120
 QY 181 TTCTGACCTGCGCTCACTACGTAACGTAACCCAGGCTGACCCAGACGCTTCAAC 180
 DB 181 TTCTGACCTGCGCTCACTACGTAACGTAACCCAGGCTGACCCAGACGCTTCAAC 180
 QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCTTAACTGCGGCGCTTTGAGCACTTT 300
 DB 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCTTAACTGCGGCGCTTTGAGCACTTT 300
 QY 301 GTCTTTGGGCTGCTGCTGTGCTGAGAGTGAAGTAAGAAATGAGACCTTTGAGGAG 360
 DB 301 GTCTTTGGGCTGCTGCTGTGCTGAGAGTGAAGTAAGAAATGAGACCTTTGAGGAG 360
 QY 361 CAACTGACGAGATTGAGATCGTGGCTTACCTGAGACACGCTGTGCTGAGATGAGAC 420
 DB 361 CAACTGACGAGATTGAGATCGTGGCTTACCTGAGACACGCTGTGCTGAGATGAGAC 420
 QY 421 AGTGGGCGCTGGCGGACTTCAACGCTTAATACGGGAGCGGGGCGCTGAGAGACGAC 480
 DB 421 AGTGGGCGCTGGCGGACTTCAACGCTTAATACGGGAGCGGGGCGCTGAGAGACGAC 480

QY 481 CGTCTGCGGAGAGGCAACTGGGCAATGATGAGACACAGTGTGACGGGGCGCTGGCACTG 540
 DB 481 CGTCTGCGGAGAGGCAACTGGGCAATGATGAGACACAGTGTGACGGGGCGCTGGCACTG 540
 QY 541 GGGGCGCTGGTAACTGTATGAGGGCGCTTTTGTCTGACAAAGTG 581
 DB 541 GGGGCGCTGGTAACTGTATGAGGGCGCTTTTGTCTGACAAAGTG 581

RESULT 5

AAV28333
 ID AAV28333 standard; cDNA; 579 BP.

AC AAV28333;

DT 02-OCT-1998 (first entry)

DE Rat bcl-y gene.

OS ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.

XX Rattus sp.

FT Key Location/Qualifiers

FT CDS 1..579

FT /tag= a "bcl-y"

FT /product= "bcl-y"

FT /note= "No stop codon given"

PN US5769201-A.

PD 04-AUG-1998.

PF 11-FEB-1997; 97US-00798897.

PR 23-FEB-1996; 96US-0012201P.

PA (COCE-) COCENSYS INC.

PI Guastella J;

DR MPI; 1998-446079/38.

DR P-PBDB; AAW61391.

PT Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing
 PT recombinant protein for use in treating uncontrolled cell growth e.g.
 XX cancers.

PS Claim 2; Column 13/14; 27pb; English.

CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
 CC family, components in the cell death pathway. The bcl-2 family have both
 CC apoptotic activity and the apoptosis blocking activity. bcl-y falls in
 CC the apoptosis activity category. The recombinant protein may be used to
 CC prevent uncontrolled cell growth. The recombinant protein may be used to
 CC recombinant genetic constructs to increase its expression in vivo. Also,
 CC antisense constructs can be used in disorders where prevention of cell
 CC death is desired

SO Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;

Query Match 93.0%; Score 540.6; DB 2; Length 579;
 Best Local Similarity 95.9%; Pred. No. 8e-137;

Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGCGAAGCCGACCTCAACCCAGACACACGCGCTCAAGTGGCTGACTTTGAGGCTAT 60
 DB 1 ATGCGAAGCCGACCTCAACCCAGACACACGCGCTCAAGTGGCTGACTTTGAGGCTAT 60
 QY 61 AGGCTGAGGACGAGAGGATTATGCTGTGAGAGCTGGGCTGGGAGAGCCGACCGGAC 120
 DB 61 AGGCTGAGGACGAGAGGATTATGCTGTGAGAGCTGGGCTGGGAGAGCCGACCGGAC 120

QY 121 CCGGTGACCAAGGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 180
XX 121 CCGGTGACCAAGGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 180
Db 121 CCGGTGACCAAGGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 180
QY 181 TTCTCTGACCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 240
XX 181 TTCTCTGACCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 240
Db 181 TTCTCTGACCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 240
QY 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGCGCTTAACTGCGGCGCTTGTGCAATTCCTT 300
XX 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGCGCTTAACTGCGGCGCTTGTGCAATTCCTT 300
Db 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGCGCTTAACTGCGGCGCTTGTGCAATTCCTT 300
QY 301 GTCTTTGGGGGCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 360
XX 301 GTCTTTGGGGGCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 360
Db 301 GTCTTTGGGGGCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 360
QY 361 CAACTGCAAGATTGATGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 420
XX 361 CAACTGCAAGATTGATGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 420
Db 361 CAACTGCAAGATTGATGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 420
QY 421 AGTGGCGGCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 480
XX 421 AGTGGCGGCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 480
Db 421 AGTGGCGGCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 480
QY 481 CGTCTGCGGAGGCGCACTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 540
XX 481 CGTCTGCGGAGGCGCACTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 540
Db 481 CGTCTGCGGAGGCGCACTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 540
QY 541 GGGGCGCTGTAATGTAAGGGGCTTTTCTGTAAGAG 579
XX 541 GGGGCGCTGTAATGTAAGGGGCTTTTCTGTAAGAG 579
Db 541 GGGGCGCTGTAATGTAAGGGGCTTTTCTGTAAGAG 579

RESULT 6
AA15945
ID AA15945 standard; cDNA; 579 BP.

XX AA15945;

XX 20-MAY-1999 (first entry)

XX cDNA encoding the rat bcl-y protein.

XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
XX multiple sclerosis; myocardial infarction; vitally induced cell death;
XX aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
XX premature cell death; cell death stimulator; prolonged cell life span;
XX Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;
XX 89.

XX Rattus sp.

XX US883229-A.

XX 16-MAR-1999.

XX 25-NOV-1997; 97US-00978523.

XX 23-FEB-1996; 96US-0012201P.

XX 11-FEB-1997; 97US-00798897.

XX (COCE-) COCENSYS INC.

XX Guestella J;

XX WPI; 1999-214150/18.

XX P-PSDB; AAW97391.

XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
XX modulating programmed cell death.

XX Disclousure; Col 13-16; 26pp; English.

XX The present sequence encodes rat bcl-y protein (Rbcl-y). The
XX specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
XX Hbcl-y are homologues of the bcl-2 protein thought to be involved in
XX programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
XX proteins may be used to treat conditions associated with a disruption of
XX the cell death pathway. If they act as cell death inhibitors, they may be
XX used in therapies to treat subjects suffering from: strokes, head trauma,
XX Alzheimer's Disease, neural and muscular degenerative diseases
XX (especially multiple sclerosis), myocardial infarction, vitally induced
XX cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
XX - conditions where cells under go premature cell death as a result of
XX triggers which may or may not be apparent. They may also be used in this
XX way to develop cell lines which remain viable in culture for an extended
XX period. In contrast, if they act as cell death stimulators, Rbcl-y and
XX Hbcl-y may be used to treat conditions associated with prolonged cell
XX life span such as cancer (especially Kaposi's sarcoma and lung cancer)
XX and auto/hyperimmune diseases. They may also be used to cause cell death
XX in, and hence control, parasites

XX Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;

XX Query Match 93.0%; Score 540.6; DB 2; Length 579;

XX Best Local Similarity 95.9%; Pred. No. 88-137;

XX Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCGAGCTTCAACCCGAGACACACGCGCTGTAAGCTGTAATTTAGGCTAT 60
XX 1 ATGCCGACCCCGAGCTTCAACCCGAGACACACGCGCTGTAAGCTGTAATTTAGGCTAT 60
Db 1 ATGCCGACCCCGAGCTTCAACCCGAGACACACGCGCTGTAAGCTGTAATTTAGGCTAT 60

QY 61 AGCTGAGAGAGAGAGGTTATGCTGAGAGAGAGGCTGAGAGAGAGAGAGAGAGAGAGAG 120
XX 61 AGCTGAGAGAGAGAGGTTATGCTGAGAGAGAGGCTGAGAGAGAGAGAGAGAGAGAGAG 120
Db 61 AGCTGAGAGAGAGAGGTTATGCTGAGAGAGAGGCTGAGAGAGAGAGAGAGAGAGAGAG 120

QY 121 CCGGTGACCAAGGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 180
XX 121 CCGGTGACCAAGGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 180
Db 121 CCGGTGACCAAGGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 180

QY 181 TTCTCTGACCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 240
XX 181 TTCTCTGACCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 240
Db 181 TTCTCTGACCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 240

QY 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGCGCTTAACTGCGGCGCTTGTGCAATTCCTT 300
XX 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGCGCTTAACTGCGGCGCTTGTGCAATTCCTT 300
Db 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGCGCTTAACTGCGGCGCTTGTGCAATTCCTT 300

QY 301 GTCTTTGGGGGCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 360
XX 301 GTCTTTGGGGGCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 360
Db 301 GTCTTTGGGGGCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 360

QY 361 CAACTGCAAGATTGATGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 420
XX 361 CAACTGCAAGATTGATGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 420
Db 361 CAACTGCAAGATTGATGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 420

QY 421 AGTGGCGGCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 480
XX 421 AGTGGCGGCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 480
Db 421 AGTGGCGGCTGCGGCTGCTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 480

QY 481 CGTCTGCGGAGGCGCACTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 540
XX 481 CGTCTGCGGAGGCGCACTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 540
Db 481 CGTCTGCGGAGGCGCACTGAGAGAGAGTTTGAAGACCCGTTTCCGGCGACCC 540

QY 541 GGGGCGCTGTAATGTAAGGGGCTTTTCTGTAAGAG 579
XX 541 GGGGCGCTGTAATGTAAGGGGCTTTTCTGTAAGAG 579
Db 541 GGGGCGCTGTAATGTAAGGGGCTTTTCTGTAAGAG 579

RESULT 7
ABV78153
ID ABV78153 standard; DNA; 582 BP.

XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
XX modulating programmed cell death.

AC ABV78153;
 XX
 DT 15-NOV-2002 (first entry)
 DE Human bcl-2 DNA SEQ ID NO 37.
 KW RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;
 KM virucide; protozoicide; gene; ds.
 OS Homo sapiens.
 PN MO200255693-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 09-JAN-2002; 2002MO-EP000152.
 PR 09-JAN-2001; 2001DE-01000586.
 PR 26-OCT-2001; 2001DE-0105280.
 PR 29-NOV-2001; 2001DE-0105841.
 PR 07-DEC-2001; 2001DE-01060151.
 XX
 PA (RIBO-) RIBOPHARMA AG.
 XX
 PI Kreutzler R, Limmer S, Rost S, Hadwiger P;
 DR WPI; 2002-590671/63.
 XX
 PT Inhibiting expression of target gene, useful e.g. for inhibiting
 PT oncogenes, by administering double-stranded RNA complementary to the
 PS target and having an overhang.
 PS Claim 10; Page 134; 203pp; German.
 XX
 CC The invention relates to inhibiting expression of a target gene (I) in a
 CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded
 CC structure of at most 49 consecutive bases. At least part of one strand
 CC (dsRNA) is complementary to (I) and at least one end of dsRNA
 CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
 CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
 CC in humans, also genes in Plasmodium or in viruses or viroids that are
 CC pathogenic for humans, animals or plants. Introducing an overhang into
 CC dsRNA greatly increases effectiveness for inhibiting gene expression, into
 CC both in vivo and in vitro and also increases stability and thus the
 CC effective concentration inside the cell. The present sequence is that of
 XX a gene related to the invention
 XX
 Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;
 Query Match 87.1%; Score 505.8; DB 6; Length 582;
 Best Local Similarity 91.9%; Pred. No. 2,3e-127;
 Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
 OY 1 ATGCCGACCCCAAGCCCTCAACCCCAAGACAGACGCGCTCTAGTGTGCTGATCTTGTAGGCTAT 60
 DB 1 ATGCCGACCCCAAGCCCTCGAGCCCAAGACAGACGCGCTCTGTGTGCAAGCTTTGTAGGCTAT 60
 OY 61 AGGCTGAGGCAAGAGGTTATGTCTGTGAGCTGGGCTGTGGGAGGCCCAAGCCGCGAC 120
 DB 61 AGGCTGAGGCAAGAGGTTATGTCTGTGAGCTGGGCTGTGGGAGGCCCAAGCCGCGAC 120
 OY 121 CCGCTGACCAAGCCATGCGGCGCTGTGAGAGAGAGATTGTGAGCCCGTTTCCGCGGAC 180
 DB 121 CCGCTGACCAAGCCATGCGGCGCTGTGAGAGAGAGATTGTGAGCCCGTTTCCGCGGAC 180
 OY 181 TTCTGTACCTGGGCGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 240
 DB 181 TTCTGTACCTGGGCGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 240
 OY 241 CAGGTTTCCAGCAACTTTTCCAGAGGGGCGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 300
 DB 241 CAGGTTTCCAGCAACTTTTCCAGAGGGGCGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 300

OY 301 GTCTTGGGGGCTGCGCTGTGTCTGTAGAGATGTCAACAAAGAAATGACCTTTGGTGGGA 360
 DB 301 GTCTTGGGGGCTGCGCTGTGTCTGTAGAGATGTCAACAAAGAAATGACCTTTGGTGGGA 360
 OY 361 CAAATCCAGAGATTTGATTCGTGCGCTTACCTGAGACAGCTGTGCTGATGATGATCAAGC 420
 DB 361 CAAATCCAGAGATTTGATTCGTGCGCTTACCTGAGACAGCTGTGCTGATGATGATCAAGC 420
 OY 421 AGTGGCGGCTGGGCGGAGCTTCAACAGCTTATACCGGAGACCGGCGCTGAGAGACCAAGC 480
 DB 421 AGTGGCGGCTGGGCGGAGCTTCAACAGCTTATACCGGAGACCGGCGCTGAGAGACCAAGC 480
 OY 481 CCGTTCGCGGAGAGGCAATGAGGCAATGAGTGTAGAGACAGTGTGTGAGAGAGAGAGAGAG 540
 DB 481 CCGTTCGCGGAGAGGCAATGAGGCAATGAGTGTAGAGACAGTGTGTGAGAGAGAGAGAGAG 540
 OY 541 GGGGCGCTGTGATCTGTAGAGGCGCTTTTGTGCTAGCAAGTG 581
 DB 541 GGGGCGCTGTGATCTGTAGAGGCGCTTTTGTGCTAGCAAGTG 581
 RESULT 8
 ID AB235729 standard; DNA; 582 BP.
 XX
 AC AB235729;
 XX
 DT 07-FEB-2003 (first entry)
 DE Human bcl-2 polynucleotide SEQ ID NO 37.
 XX
 KW Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
 KW protozoicide; gene expression; antisense; tumour; infection; Plasmodium;
 KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
 XX Hepatitis C virus; human papilloma virus; gene; ds.
 OS Homo sapiens.
 XX
 XX DE10100586-A1.
 XX
 PD 18-JUL-2002.
 XX
 PF 09-JAN-2001; 2001DE-01000586.
 PR 09-JAN-2001; 2001DE-01000586.
 PR 09-JAN-2001; 2001DE-01000586.
 XX
 PI (RIBO-) RIBOPHARMA AG.
 XX
 DR Kreutzler R, Limmer S, Rost S, Hadwiger P;
 XX
 PT Inhibiting expression of target genes, useful e.g. for treating tumors,
 PT by introducing into cells two double-stranded RNAs that are complementary
 PS to the target.
 PS Claim 13; Page 30-31; 100pp; German.
 XX
 CC The invention relates to inhibiting expression of a target gene in a cell
 CC by introducing at least two oligonucleotides (dsRNA and II), both
 CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
 CC pairs. At least part of one strand (SI, S2) of the ds structures in each
 CC method uses antisense inhibition to regions in the target gene. The
 CC RNA inhibition (RNAi). The method is particularly used to treat tumours
 CC or infections, especially by Plasmodium or viruses/viroids (pathogenic
 CC humans, animals or plants). The method provides more effective inhibition
 CC of expression than known methods using a single dsRNA, even at very low
 CC concentrations. When dsRNA has at least one unpaired nucleotide at the
 CC end and stability (and thus effective concentration in the cell) is improved
 CC and efficiency can be increased further by pretreating the cells with
 CC interferon. The present sequence is that of a target DNA of the invention
 XX

ABL91694
ID ABL91694 standard; DNA; 582 BP.

AC ABL91694;

DT 28-MAY-2002 (first entry)

DE Human polynucleotide SEQ ID NO 37.

XX Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KM Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
XX Cystostatic; virucide; protozoicide; antibacterial; ds.
OS Homo sapiens.

PN DE10100586-CL.

PD 11-APR-2002.

PF 09-JAN-2001; 2001DE-01000586.

PR 09-JAN-2001; 2001DE-01000586.

PA (RIBO-) RIBOPHARMA AG.

PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
DR WPI; 2002-270454/32.

PT Inhibiting gene expression in cells, useful for e.g. treating tumours, by
PT introducing double-stranded complementary oligonucleotides having unpaired
XX terminal bases.

PS Claim 13; Page 32; 104pp; German.

CC The invention relates to a method for inhibiting expression of a target
CC gene (ABL91658-ABL91797) in a cell by introducing at least one
CC oligoribonucleotide that has a double-stranded structure consisting of at
CC most 49 sequential nucleotide pairs, with at least part of one strand
CC complementary with the target gene and has at least one end a single-
CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for
CC antisense inhibition of gene expression useful e.g. for treating tumours
CC but the oligoribonucleotides may also be directed against genes present
CC in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans,
CC animals or plants) or against cytokine, id, developmental or prion genes.
CC The method provides more effective inhibition of gene expression than use
CC of known oligonucleotides, probably because the unpaired overhang
CC increases stability and thus intracellular concentration

Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match Best Local Similarity 87.1%; Score 505.8; DB 6; Length 582;
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCGCTCAACCCGACACACACGCTCTAGTGTGCTGATTTGGAGGCTAT 60
DB 1 ATGGGACCCCGCTCGGCCCCAGACACACGCGCTCTGTGGCACAATTGTGAGGTAT 60
QY 61 AGCGTGAAGCGAAGGTTATGTCTGTGAGCTGGCGCTGGGGAAGCCCGACCGGAC 120
DB 61 AAGCTGAGGCGAAGGTTATGTCTGTGAGCTGGCGCTGGGGAAGCCCGACCGGAC 120
QY 121 CGCGTGAACCAAGCAAGCGGCTGTGAGACAGATTGAGACCCGTTTCCGCGGACAC 180
DB 121 CGCGTGAACCAAGCAAGCGGCTGTGAGACAGATTGAGACCCGTTTCCGCGGACAC 180
QY 181 TTCTCTGACTGCGCTGCTAGCTACACGTCGACCCAGGCTGACCGCAACGCTTACC 240
DB 181 TTCTCTGACTGCGCTGCTAGCTACACGTCGACCCAGGCTGACCGCAACGCTTACC 240
QY 241 CAGGTTCCGACGAATTTTCAAGGGGCGCTTAACGCGGCGCTTGTGGGCAATCTTT 300
DB 241 CAGGTTCCGACGAATTTTCAAGGGGCGCTTAACGCGGCGCTTGTGGGCAATCTTT 300

DB 241 CAGGTTCCGACGAATTTTCAAGGGGCGCTTAACGCGGCGCTTGTGGGCAATCTTT 300
QY 301 GTCTTTGGGAGCTGCGCTGTGTGCTGAGAGTGCACAAAGAAATGAGACCTTTGGTGA 360
DB 301 GTCTTTGGGAGCTGCACTGTGTCTGAGAGTGCACAAAGAAATGAGACCTTTGGTGA 360
QY 361 CAAATCCAGGATTTGAGATGCTGCTGCTGCTGAGACACAGTGTGCTGCTGATTCACAC 420
DB 361 CAAATCCAGGATTTGAGATGCTGCTGCTGCTGAGACACAGTGTGCTGCTGATTCACAC 420
QY 421 AAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 AAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CGCTGCGGAGAGGCACTGCGGCAATGAGTACACAGTGTGACGCGGCGCTGAGAGCGCGG 480
DB 481 CGCTGCGGAGAGGCACTGCGGCAATGAGTACACAGTGTGACGCGGCGCTGAGAGCGCGG 480
QY 541 GGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 541 GGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

RESUIT 11
AAK25132
ID AAK25132 standard; DNA; 581 BP.

AC AAK25132;

DT 05-JUL-1999 (first entry)

DE Human bcl-w gene.

XX Spermatoogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
KM animal model; ss.

OS Homo sapiens.

PN WO9913710-A1.

PD 25-MAR-1999.

PF 16-SEP-1998; 98WO-AU000764.

PR 16-SEP-1997; 97AU-00009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PI Cory S, Adams J, Print C, Gibson L, Koentgen F;

DR WPI; 1999-243890/20.

DR P-PDB; AAY05530.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or

PS protein associated with Bcl-w.

Claim 3; Page 32; 52pp; English.
CC The present sequence is the human bcl-w gene encoding Bcl-w protein (see
CC AAY05530), a pro-survival member of the Bcl-2 family which is widely
CC expressed and which is essential for spermatogenesis. The invention
CC relates generally to a method of treatment and to an animal model for
CC identification of molecules and genetic sequences useful for inducing or
CC reducing fertility of male animals. Methods are provided for inducing or
CC treatment of infertility, or for reducing fertility, by modulating
CC spermatogenesis. An animal model carries a mutation in at least one
CC allele of the human or murine bcl-w gene or in a gene associated with bcl
CC -w. Such animals have disorganised seminiferous tubules and are
CC substantially infertile, but possess no other major abnormalities as
CC determined by histological examination. They can be used to screen for
CC enhancing or otherwise facilitating genetic sequences capable of inducing,
CC can induce infertility

XX Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other;
SQ

Query Match 86.5%; Score 502.6; DB 2; Length 581;
Best Local Similarity 91.6%; Pred. No. 1.7e-126;

Matches 532; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

```

QY 1 ATGCGAGCCCGAGCTCAACCCAGACACAGCGGCTGAGTGGCTTGTGAGGCTAT 60
DB 1 ATGCGAGCCCGAGCTCAACCCAGACACAGCGGCTGAGTGGCTTGTGAGGCTAT 60
QY 61 AGGCTGAGGAGGAGGTTATGCTGTGAGTCACTGCGGCTGCGGAGGCGCCAGCCGAC 120
DB 61 AGGCTGAGGAGGAGGTTATGCTGTGAGTCACTGCGGCTGCGGAGGCGCCAGCGTAC 120
QY 121 CCGCTGACCAAGCCATGCGGCGCTGCTGAGACAGATTGAGACCCGTTCCGCGCAC 180
DB 121 CCGCTGACCAAGCCATGCGGCGCTGCTGAGATGATGAGACCCGCTTCGCGCAC 180
QY 181 TTCTCTGACCTGCGGCTGAGCTACAGTGAAGCCAGGCTGAGCCAGCAAGCTTAC 240
DB 181 TTCTCTGATCTGCGGCTGAGCTACAGTGAAGCCAGGCTGAGCCAGCAAGCTTAC 240
QY 241 CAGGTTCCGAGCACTTTTCCAAAGGCGGCTTAAGTGGGCGCTTGTGAGTCTTT 300
DB 241 CAGGTTCCGAGTGAATTTTCCAAAGGCGGCTTAAGTGGGCGCTTGTGAGTCTTT 300
QY 301 GTCCTTGGGCGCTGCTGCTGTGCTGAGAGTGTCAACAAAGATGAGCTTGTGGGA 360
DB 301 GTCCTTGGGCGCTGCTGCTGTGCTGAGAGTGTCAACAAAGATGAGCTTGTGGGA 360
QY 361 CAAATCCAGAGTTGGATCTGTGCGCTTACCTGAGACAGTGTGGGCTGAGTGTCAAC 420
DB 361 CAAATCCAGAGTTGGATCTGTGCGCTTACCTGAGACAGTGTGGGCTGAGTGTCAAC 420
QY 421 AGTGGCGGCTGCGGCGGACTTCAAGCTTATACGCGGAGCGGCGCTGAGTGTCAAC 480
DB 421 AGTGGCGGCTGCGGCGGACTTCAAGCTTATACGCGGAGCGGCGCTGAGTGTCAAC 480
QY 481 CGTCTGCGGAGGAGCACTGCGGATGAGTGAACAGTGTGACGCGGCGCTGAGTGT 540
DB 481 CGTCTGCGGAGGAGCACTGCGGATGAGTGAACAGTGTGACGCGGCGCTGAGTGT 540
QY 541 GGGGCGCTGCTGTAATGTAGGGGCTTTTGTGCTAGCAAGTG 581
DB 541 GGGGCGCTGCTGTAATGTAGGGGCTTTTGTGCTAGCAAGTG 581

```

RESULT 12

ABT16642 standard; DNA; 3542 BP.

AC ABT16642;

DT 03-APR-2003 (first entry)

DE Human bcl-2 gene SEQ ID No 4.

XX Anti-tumour; DNAzyme; bcl-2 gene; tumour; malignant; chemotherapy;
XX radiation therapy; catalytic domain; enzyme; human; ds.

OS Homo sapiens.

XX W0200299090-A1.

XX 12-DEC-2002.

PF 07-JUN-2002; 2002MO-AU000739.

PR 07-JUN-2001; 2001AU-00005527.

PA (JOHN) JOHNSON & JOHNSON RES PTY LTD.

XX

PI Sun L, Wang L, Turner RJ, Saravolac EG, Dass CR;
XX WPI; 2003-140617/13.

PT Novel DNAzyme useful for treating tumors, and for enhancing the
XX sensitivity of malignant or virus infected cells to therapy, comprises a
PT catalytic domain and binding domain contiguous to the catalytic domain.

PS Disclosure; Page 44-45; 67pp; English.

XX The invention relates to a DNAzyme which specifically cleaves mRNA
CC transcribed from a member of the bcl-2 gene family. The DNAzymes comprise
CC a catalytic domain, binding domains contiguous with the 5' and 3' end of
CC the catalytic domain, and therefore hybridise with, the two regions
CC immediately flanking the purine residue of the cleavage site within the
CC bcl-2 gene family mRNA, at which DNAzyme-catalysed cleavage is desired. A
CC pharmaceutical composition comprising a DNAzyme of the invention is
CC useful for treating tumours in a subject, and for enhancing the
CC sensitivity of malignant or virus infected cells infected cells to
CC therapy. The DNAzymes are useful in diagnostics, therapeutics,
CC prophylaxis, research agents and in kits. The DNAzymes are also useful
CC for increasing the susceptibility of tumour cells to anti-tumour
CC therapies such as chemotherapy and radiation therapy. This polynucleotide
CC sequence represents a human bcl-2 gene of the invention

SQ Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;

Query Match 86.5%; Score 502.6; DB 8; Length 3542;

Best Local Similarity 91.6%; Pred. No. 3e-126;
Matches 532; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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QY 1 ATGCGAGCCCGAGCTCAACCCAGACACAGCGGCTGAGTGGCTTGTGAGGCTAT 60
DB 1 ATGCGAGCCCGAGCTCAACCCAGACACAGCGGCTGAGTGGCTTGTGAGGCTAT 60
QY 177 ATGCGAGCCCGAGCTCAACCCAGACACAGCGGCTGAGTGGCTTGTGAGGCTAT 236
DB 177 ATGCGAGCCCGAGCTCAACCCAGACACAGCGGCTGAGTGGCTTGTGAGGCTAT 236
QY 61 AGGCTGAGGAGGAGGTTATGCTGTGAGTCACTGCGGCTGCGGAGGCGCCAGCCGAC 120
DB 61 AGGCTGAGGAGGAGGTTATGCTGTGAGTCACTGCGGCTGCGGAGGCGCCAGCGTAC 120
QY 237 AAGCTGAGGAGGAGGTTATGCTGTGAGTCACTGCGGCTGCGGAGGCGCCAGCGTAC 296
DB 237 AAGCTGAGGAGGAGGTTATGCTGTGAGTCACTGCGGCTGCGGAGGCGCCAGCGTAC 296
QY 297 CCGCTGACCAAGCCATGCGGCGCTGCTGAGACAGATTGAGACCCGTTCCGCGCAC 356
DB 297 CCGCTGACCAAGCCATGCGGCGCTGCTGAGACAGATTGAGACCCGTTCCGCGCAC 356
QY 357 TTCTCTGATCTGCGGCTGAGCTACAGTGAAGCCAGGCTGAGCCAGCAAGCTTAC 416
DB 357 TTCTCTGATCTGCGGCTGAGCTACAGTGAAGCCAGGCTGAGCCAGCAAGCTTAC 416
QY 417 CAGGTTCCGAGCACTTTTCCAAAGGCGGCTTAAGTGGGCGCTTGTGAGTCTTT 476
DB 417 CAGGTTCCGAGTGAATTTTCCAAAGGCGGCTTAAGTGGGCGCTTGTGAGTCTTT 476
QY 477 GTCCTTGGGCGCTGCTGCTGTGCTGAGAGTGTCAACAAAGATGAGCTTGTGGGA 536
DB 477 GTCCTTGGGCGCTGCTGCTGTGCTGAGAGTGTCAACAAAGATGAGCTTGTGGGA 536
QY 537 CAAATCCAGAGTTGGATCTGTGCGCTTACCTGAGACAGTGTGAGCTGAGTGTCAAC 596
DB 537 CAAATCCAGAGTTGGATCTGTGCGCTTACCTGAGACAGTGTGAGCTGAGTGTCAAC 596
QY 597 AGTGGCGGCTGCGGCGGACTTCAAGCTTATACGCGGAGCGGCGCTGAGTGTCAAC 656
DB 597 AGTGGCGGCTGCGGCGGACTTCAAGCTTATACGCGGAGCGGCGCTGAGTGTCAAC 656
QY 657 CGTCTGCGGAGGAGCACTGCGGATGAGTGAACAGTGTGACGCGGCGCTGAGTGT 716
DB 657 CGTCTGCGGAGGAGCACTGCGGATGAGTGAACAGTGTGACGCGGCGCTGAGTGT 716
QY 717 GGGGCGCTGCTGTAATGTAGGGGCTTTTGTGCTAGCAAGTG 757
DB 717 GGGGCGCTGCTGTAATGTAGGGGCTTTTGTGCTAGCAAGTG 757

```

RESULT 13

AA96577
 ID AA96577 standard; DNA; 583 BP.
 AC AA96577;
 DT 22-APR-1998 (first entry)
 XX
 XX Human bcl-w DNA.
 DE
 KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 KW diagnosis; degenerative disease; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..582
 FT /tag= a
 FT /product= "bcl-w"
 XX
 XX MO9735971-A1.
 XX
 PD 02-OCT-1997.
 XX
 PF 27-MAR-1997; 97MO-AU000199.
 XX
 PR 27-MAR-1996; 96AU-00008965.
 XX
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 PI Cory S, Adams JM, Gibson LM, Holmgreen SP;
 XX
 DR WPI; 1997-489635/45.
 DR P-PSDB; AAM36047.
 XX
 XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
 PT inhibit cell survival, e.g. for treatment of cancer and degenerative
 PT diseases.
 XX
 PS Claim 3; Page 48; 86pp; English.
 XX
 CC This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
 CC family, extracted from an adult brain library. This gene promotes cell
 CC survival, so its modulation is useful in treatment of cancer or auto-
 CC immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease,
 CC myocardial infarct, muscular degeneration, hypoxia, ischaemia, human
 CC immunodeficiency virus infection or in cell transplants. Up-regulation of
 CC the gene can also be used to modify cell lines cultured in vivo, e.g. to
 CC develop new lines, to facilitate isolation of hybridomas and to increase
 CC survival of primary explants during genetic modification. It can be used
 CC or screening of potential modulators
 CC
 SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;
 Query Match 86.2%; Score 501; DB 2; Length 583;
 Best Local Similarity 91.4%; Pred. No. 4.7e-126;
 Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 1 ATGCGACCCGAGCTTAACTCCAGACACGCGCTCTAGTGGCTGACTTTGAGGCTAT 60
 DB 1 ATGCGACCCGAGCTTAACTCCAGACACGCGCTCTAGTGGCTGACTTTGAGGCTAT 60
 QY 61 AGGCTGAGGAGGAAGGCTTATGCTGTGAGAGCTGGGCTGGGGAAAGCCGACCCGAC 120
 DB 61 AAGCTGAGGAGGAAGGCTTATGCTGTGAGAGCTGGGCTGGGGAAAGCCGACCACTGAC 120
 QY 121 CCGGTGACCAAGCAAGTGGGCTGCTGTGAGAGCAAGTTTGAACCCGTTTCCGCGACAC 180
 DB 121 CCGGTGACCAAGCAAGTGGGCTGCTGTGAGAGCAAGTTTGAACCCGTTTCCGCGACAC 180
 QY 121 CCGGTGACCAAGCAAGTGGGCTGCTGTGAGAGCAAGTTTGAACCCGTTTCCGCGACAC 180
 DB 121 CCGGTGACCAAGCAAGTGGGCTGCTGTGAGAGCAAGTTTGAACCCGTTTCCGCGACAC 180
 QY 181 TTCTTGACCTGGCCCTCAGCTACAGCAGCCCAAGGCTCAGCCAGCAAGCTTCAAC 240
 DB 181 TTCTTGACCTGGCCCTCAGCTACAGCAGCCCAAGGCTCAGCCAGCAAGCTTCAAC 240
 DB 181 TTCTTGACCTGGCCCTCAGCTACAGCAGCCCAAGGCTCAGCCAGCAAGCTTCAAC 240

QY 241 CAGTTTCCGAGCAAGATTTCACAGGGGCGCCCTAACTGGGGCGCTTTGGGCAATCTTT 300
 DB 241 CAGTTTCCGAGCAAGATTTCACAGGGGCGCCCTAACTGGGGCGCTTTGGGCAATCTTT 300
 QY 301 GCTTTGGGCGCTCCCTGTGTGTGAGAGTGTCAACAAGAAATGAGCCCTTTGGGGA 360
 DB 301 GCTTTGGGCGCTCCCTGTGTGTGAGAGTGTCAACAAGAAATGAGCCCTTTGGGGA 360
 QY 361 CAAGTCCAGCAATGATGTGGGCTTACCTGAGACACAGTGTGCTGATCCAGAC 420
 DB 361 CAAGTCCAGCAATGATGTGGGCTTACCTGAGACACAGTGTGCTGATCCAGAC 420
 QY 421 AGTGGCGGCTGGGCGGACTTCAAGCTCTATACGGGAGCGGGCCCTGGAGGACCAAG 480
 DB 421 AGTGGCGGCTGGGCGGACTTCAAGCTCTATACGGGAGCGGGCCCTGGAGGACCAAG 480
 QY 481 CGTCTGGGAGGAGCACTGGGATGAGAGACAGTGTGTACAGGGGCGCTGGCACTG 540
 DB 481 CGTCTGGGAGGAGCACTGGGATGAGAGACAGTGTGTACAGGGGCGCTGGCACTG 540
 QY 541 GGGGCGCTGGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
 DB 541 GGGGCGCTGGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
 RESULT 14
 AAX25134
 ID AAX25134 standard; DNA; 583 BP.
 XX
 AC AAX25134;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human bcl-w gene derivative.
 KW
 KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
 KW animal model; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9913710-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 16-SEP-1998; 98MO-AU000764.
 XX
 PR 16-SEP-1997; 97AU-00009228.
 XX
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX
 PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
 XX
 DR WPI; 1999-243890/20.
 DR P-PSDB; AAY05532.
 XX
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 PS
 PS Disclosure; Page 36; 52pp; English.
 XX
 CC The present sequence is described as a derivative of the human bcl-w gene
 CC (see AAX25132) and encodes Bcl-w protein (see AAY05532), a pro-survival
 CC member of the Bcl-2 family which is widely expressed and which is
 CC essential for spermatogenesis. The invention relates generally to a
 CC method of treatment and to an animal model for the identification of
 CC molecules and genetic sequences useful for inducing or reducing fertility
 CC of male animals. Methods are provided for the treatment of infertility
 CC or for reducing fertility, by modulating spermatogenesis. An animal model
 CC carries a mutation in at least one allele of the human or murine bcl-w
 CC gene or in a gene associated with bcl-w. Such animals have disorganised
 CC seminiferous tubules and are substantially infertile, but possess no other
 CC major abnormalities as determined by histological examination. They can

be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility

SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;

| Query Match | Score | DB 2 | Length | 583 |
|-------------|-------|------|--------|-----|
| 86.2% | 501 | | | |

Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

[illegible]

```

RESULT 15
AAV28334
ID AAV28334 standard; cDNA; 579 BP

```

AC AAV28334,

DT 02-OCT-1998 (first entry)

Human *bcl-2* gene.

KW ss; bcl-1-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

OS Homo sapiens.

| FH | Key | Location/Qualifiers |
|----|-----|---------------------|
| 1 | 200 | 100 |

/*tag=

/notes= "No stop codon given"

PN US5789201-A.

PD 04-AUG-1998

PF 11-FEB-1997; 97US-00798897.

PR 23-FEB-1996; 96US-0012201P.

PA (COCE-) COCENSYS INC.

PI Guastella J;

DR WPI; 1998-446079/38

XX

PT recombinant protein for use in treating uncontrolled cell growth e.g.

PS Claim 3; Column 15/16; 27pp; English

The mammalian bcl-2 genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-2 falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired

SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;

| Query Match | 85.6% | Score 497.4 | DB 2 | Length 579 |
|-------------|-------|-------------|------|------------|
|-------------|-------|-------------|------|------------|

Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | ATGCGAGCCCCAGGCTCAACCCCAAGACACAGCGCTCTAAGTGGCTGACCTTTGTAGGCTAT | 60 |
| | | | |
| Db | 1 | ATGGCGAGCCCCAGGCTCGGCCCCAGACACAGGGCTCTGTGTGGAAGACTTTTGTAGTTAT | 60 |
| QY | 61 | AGGCTGAGGCGAAGGGTTATGTCTGTGAGACTGGGACCTGGGGAGAGCCCGCCGAC | 120 |
| | | | |
| Db | 61 | AAGCTGAGGCGAAGGGTTATGTCTGTGAGACTGGCCCCGGGGAGAGGCCCAAGCTGAC | 120 |
| QY | 121 | CCGCTGCAACCAAGCCATGCGGGCTGTGGAAGCAGATTGAGACCCGTTTCCGCCGACCC | 180 |
| | | | |
| Db | 121 | CCACTGCAACCAAGCCATGCGGGCAGCTGGAATGATTCAGAACCCGCTTCCGGCGCACCC | 180 |
| QY | 181 | TTCTCTAACCCTGGCCGCTCAGCTGACAGTGAACCCAGGCTCAGGCCAGCAAGCTTACCC | 240 |
| | | | |
| Db | 181 | TTCTCTAATCTGGGGGCTCAGCTGATATGTGAACCCAGGCTCAGGCCCAAGGCTTACACC | 240 |
| QY | 241 | CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTTAACCTGGGGCCGTCTGTGGACTTCCTT | 300 |
| | | | |
| Db | 241 | CAGGTTCTCCATGAACTTTTCCAAAGGGGGCCCAACCTGGGGCCGCTGTGACCTTCTTT | 300 |
| QY | 301 | GTCCTTTGGGGCTGCCCTGTGTGCTGAGAGGTCAAACAAGAAATGAGCCTTTGGTGGGA | 360 |
| | | | |
| Db | 301 | GTCCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAAACAAGGAGATGAAACCACTGGTGGGA | 360 |
| QY | 361 | CAAACTCCAGATTTGGATCTGTGGCCCTACCTGGAGACAGCTGGGCTGACGTGATTCACAGCC | 420 |
| | | | |
| Db | 361 | CAAACTGACAGGATGTGATGTGTGGCCCTACCTGGAGAGCGCGCTGGCTGATCTGATTCACAGCC | 420 |
| QY | 421 | AGTGGCGGCTTGGGGGAGCTTCAACAGCTTATACGGGGAGCGGGGCCCTGGAGGAGCGCGG | 480 |
| | | | |
| Db | 421 | AGTGGGGGCTTGGGGGAGTTCAACAGCTTATACGGGGAGCGGGGCCCTGGAGGAGCGCGG | 480 |
| QY | 481 | CGTCTGCGGAGGGCAACTGGGCAATGAGTGAAGACAGTGTGACCGGGGACCGTGGCATCTG | 540 |
| | | | |
| Db | 481 | CGTCTGCGGAGGGGAACCTGGGCAATCAGTGAAGACAGTGTGACCGGGGACCGTGGCACTG | 540 |
| QY | 541 | GGGGCCCTGTGTACTGTAGGGGCCCTTTTTCCTAGCAAG | 579 |
| | | | |
| Db | 541 | GGGGCCCTGTGTACTGTAGGGGCCCTTTTTCCTAGCAAG | 579 |

Mon Apr 11 12:21:54 2005

Search completed: April 10, 2005, 16:55:36
Job time : 457.215 secs

us-09-925-674b-8.rng

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: April 10, 2005, 16:31:16 ; Search time 143.753 Seconds

(without alignments)
6613.285 Million cell updates/sec

Title: US-09-925-674B-8

Perfect score: 1 atgcgcagccagccctcac.....gctttttctagcaagtg 581

Sequence: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents NA.*

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|--------------------|
| 1 | 581 | 100.0 | 581 | US-09-155-327G-8 | Sequence 8, Appl1 |
| 2 | 540.6 | 93.0 | 579 | US-08-798-897-1 | Sequence 1, Appl1 |
| 3 | 540.6 | 93.0 | 579 | US-08-978-523-1 | Sequence 1, Appl1 |
| 4 | 501 | 86.2 | 582 | US-09-949-016-5057 | Sequence 5057, Ap |
| 5 | 501 | 86.2 | 583 | US-09-155-327G-6 | Sequence 6, Appl1 |
| 6 | 497.4 | 85.6 | 579 | US-08-798-897-2 | Sequence 2, Appl1 |
| 7 | 497.4 | 85.6 | 579 | US-08-798-897-2 | Sequence 2, Appl1 |
| 8 | 364.8 | 62.8 | 1098 | US-09-010-147B-23 | Sequence 23, Appl1 |
| 9 | 364.4 | 62.7 | 1864 | US-09-149-476-130 | Sequence 130, App |
| 10 | 364.2 | 62.7 | 5199 | US-09-949-016-16799 | Sequence 16799, A |
| 11 | 357 | 61.4 | 601 | US-09-949-016-177003 | Sequence 177003, A |
| 12 | 134.6 | 23.2 | 926 | US-08-081-448-5 | Sequence 5, Appl1 |
| 13 | 134.6 | 23.2 | 926 | US-08-470-670A-6 | Sequence 6, Appl1 |
| 14 | 134.6 | 23.2 | 926 | US-08-481-739-1 | Sequence 1, Appl1 |
| 15 | 134.6 | 23.2 | 926 | US-09-157-921-1 | Sequence 1, Appl1 |
| 16 | 134.6 | 23.2 | 926 | US-09-277-020-39 | Sequence 39, Appl1 |
| 17 | 134.6 | 23.2 | 926 | US-09-323-743-1 | Sequence 1, Appl1 |
| 18 | 134.6 | 23.2 | 926 | US-08-461-511A-6 | Sequence 6, Appl1 |
| 19 | 134.6 | 23.2 | 926 | US-09-021-014A-6 | Sequence 6, Appl1 |
| 20 | 134.6 | 23.2 | 926 | US-09-023-655-1430 | Sequence 1430, Ap |
| 21 | 134.6 | 23.2 | 926 | US-09-814-915A-106 | Sequence 106, App |
| 22 | 134.6 | 23.2 | 926 | PCT-US94-07089-6 | Sequence 6, Appl1 |
| 23 | 134.6 | 23.2 | 1236 | US-09-639-245-1 | Sequence 1, Appl1 |
| 24 | 130.6 | 22.5 | 1455 | US-09-639-245-7 | Sequence 7, Appl1 |
| 25 | 126.8 | 21.8 | 60489 | US-09-949-016-16287 | Sequence 16287, A |
| 26 | 125 | 21.5 | 717 | US-08-465-485A-20 | Sequence 20, Appl1 |
| 27 | 125 | 21.5 | 717 | US-09-080-285-20 | Sequence 20, Appl1 |

| | | | | | | |
|----|-------|------|------|---|--------------------|--------------------|
| 28 | 125 | 21.5 | 4825 | 6 | 5459251-1 | Patent No. 5459251 |
| 29 | 125 | 21.5 | 4825 | 6 | 5459251-1 | Patent No. 5459251 |
| 30 | 125 | 21.5 | 5086 | 2 | US-08-465-485A-19 | Sequence 19, Appl1 |
| 31 | 125 | 21.5 | 5086 | 2 | US-08-365-486A-14 | Sequence 14, Appl1 |
| 32 | 125 | 21.5 | 5086 | 3 | US-09-080-285-19 | Sequence 19, Appl1 |
| 33 | 125 | 21.5 | 5086 | 3 | US-08-880-342-14 | Sequence 14, Appl1 |
| 34 | 125 | 21.5 | 5086 | 3 | US-09-724-426-19 | Sequence 19, Appl1 |
| 35 | 125 | 21.5 | 5086 | 3 | US-09-233-527-7 | Sequence 7, Appl1 |
| 36 | 125 | 21.5 | 5086 | 5 | PCT-US93-05651-4 | Sequence 4, Appl1 |
| 37 | 125 | 21.5 | 5086 | 5 | PCT-US93-05651-2 | Sequence 2, Appl1 |
| 38 | 125 | 21.5 | 5094 | 3 | US-09-234-186-7 | Sequence 7, Appl1 |
| 39 | 125 | 21.5 | 5104 | 6 | 5506344-1 | Patent No. 5506344 |
| 40 | 125 | 21.5 | 5104 | 6 | 5506344-1 | Patent No. 5506344 |
| 41 | 125 | 21.5 | 6030 | 4 | US-09-023-655-1015 | Sequence 1015, Ap |
| 42 | 123.4 | 21.2 | 760 | 1 | US-08-405-702A-11 | Sequence 11, Appl1 |
| 43 | 123.4 | 21.2 | 1846 | 2 | US-08-365-486A-16 | Sequence 16, Appl1 |
| 44 | 123.4 | 21.2 | 1846 | 3 | US-08-880-342-16 | Sequence 16, Appl1 |
| 45 | 121.8 | 21.0 | 711 | 4 | US-09-741-238-1 | Sequence 1, Appl1 |

ALIGNMENTS

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RESULT 1
US-09-155-327G-8
Sequence 8, Application US/09155327G
Patent No. 6790637
GENERAL INFORMATION:
APPLICANT: AMRAD Operations Pty Ltd
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
FILE REFERENCE: 2096584
CURRENT FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PM965
PRIOR FILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 581
TYPE: DNA
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(579)
US-09-155-327G-8
Query Match 100.0%; Score 581; DB 4; Length 581;
Best Local Similarity 100.0%; Pred. No. 7.5e-162;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCGACCCGAGGCTTGAACCCAGACACGCGCTTGAAGCTTGAAGCTTAT 60
1 ATGCGACCCGAGGCTTGAACCCAGACACGCGCTTGAAGCTTGAAGCTTAT 60
Db 1 ATGCGACCCGAGGCTTGAACCCAGACACGCGCTTGAAGCTTGAAGCTTAT 60
QY 61 AGCGTGAAGGAGGCTTGAACCCAGACACGCGCTTGAAGCTTGAAGCTTAT 120
61 AGCGTGAAGGAGGCTTGAACCCAGACACGCGCTTGAAGCTTGAAGCTTAT 120
Db 61 AGCGTGAAGGAGGCTTGAACCCAGACACGCGCTTGAAGCTTGAAGCTTAT 120
QY 121 CCGGTGACCAACGATGCGGCTGAGAGAGGATTTGAGACCCGTTCCGCGAC 180
121 CCGGTGACCAACGATGCGGCTGAGAGAGGATTTGAGACCCGTTCCGCGAC 180
Db 121 CCGGTGACCAACGATGCGGCTGAGAGAGGATTTGAGACCCGTTCCGCGAC 180
QY 181 TTCTGTACCTGGCGCTGAGCTAAGCTAAGCTAAGCTAAGCTAAGCTTAC 240
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Db 181 TTCTGTACCTGGCGCTGAGCTAAGCTAAGCTAAGCTAAGCTTAC 240
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241 CAGTTTCCAGCAATTTTCCAGAGGAGGCTTAACTGGGCGCTTGGGCACTTTT 300
Db 241 CAGTTTCCAGCAATTTTCCAGAGGAGGCTTAACTGGGCGCTTGGGCACTTTT 300
QY 301 GTCTTGGGCGCTGCTGTGCTGAAGTGAACAAAGAAATGAGCCTTGGTGGGA 360
301 GTCTTGGGCGCTGCTGTGCTGAAGTGAACAAAGAAATGAGCCTTGGTGGGA 360
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Db 301 GTCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGATGACCTTTGGTGGGA 360
Qy 361 CAACTCCAGAGATTGATGATGAGGCTTACCTGAGACACAGTCTGGCTGACTGATCCACAGC 420
Db 361 CAACTCCAGAGATTGATGATGATGAGGCTTACCTGAGACACAGTCTGGCTGACTGATCCACAGC 420
Qy 421 AGTGGCGGCTGGGGGAGCTTACAGCTCTATACGGGGGACGGGGGCTGGAGAGACGACGCG 480
Db 421 AGTGGCGGCTGGGGGAGCTTACAGCTCTATACGGGGGACGGGGGCTGGAGAGACGACGCG 480
Qy 481 CGTCTGGGGGAGGGCAACTGGGCACTGATGAGCAACAGTGTGAGCGGGGCGGTGCACTG 540
Db 481 CGTCTGGGGGAGGGCAACTGGGCACTGATGAGCAACAGTGTGAGCGGGGCGGTGCACTG 540
Qy 541 GGGGCCCTGTGTAAGTGTGAGGGGCTTTTGTCTAGCAAGT 581
Db 541 GGGGCCCTGTGTAAGTGTGAGGGGCTTTTGTCTAGCAAGT 581

RESULT 2

US-08-798-897-1
; Sequence 1, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-08-798-897-1

Query Match 93.0%; Score 540.6; DB 1; Length 579;
Best Local Similarity 95.9%; Pred. No. 6,6e-150;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1 ATGCGACCCCAAGCTCAACCCAGACACAGCGGCTGTAGTGTGACTTTGTAGGCTAT 60
Db 1 ATGCGACCCCAAGCTCAACCCAGACACAGCGGCTGTAGTGTGACTTTGTAGGCTAT 60
Qy 61 AGCTGAGGAGCAAGGTTATGCTGTGAGAGCTGGGCTGGGGAGGCGCCAGCCGAC 120
Db 61 AGCTGAGGAGCAAGGTTATGCTGTGAGAGCTGGGCTGGGGAGGCGCCAGCCGAC 120
Qy 121 CCGTGACACCAAGCATCGGGCTGTGAGAGAGATTGAGACCCGTTTCGCGCAC 180

Db 121 CCGTGACACCAAGCATCGGGCTGTGAGAGAGATTGAGACCCGTTTCGCGCAC 180
Qy 181 TTCTTGACCTGGGCGGCTCACTACGTGACATGTAACCCAGGCTCAGCCAGCAAGCTTACC 240
Db 181 TTCTTGACCTGGGCGGCTCACTACGTGACATGTAACCCAGGCTCAGCCAGCAAGCTTACC 240
Qy 241 CAGTTTCCAGCAAGATTTCCTTCAAGGGGGGCGCTTACTGAGGGGCGTCTTGGGCACTTCTT 300
Db 241 CAGTTTCCAGCAAGATTTCCTTCAAGGGGGGCGCTTACTGAGGGGCGTCTTGGGCACTTCTT 300
Qy 301 GTCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGATGACCTTTGGTGGGA 360
Db 301 GTCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGATGACCTTTGGTGGGA 360
Qy 361 CAACTCCAGAGATTGATGATGATGAGGCTTACCTGAGACACAGTCTGGCTGACTGATCCACAGC 420
Db 361 CAACTCCAGAGATTGATGATGATGAGGCTTACCTGAGACACAGTCTGGCTGACTGATCCACAGC 420
Qy 421 AGTGGCGGCTGGGGGAGCTTACAGCTCTATACGGGGGACGGGGGCTGGAGAGACGACGCG 480
Db 421 AGTGGCGGCTGGGGGAGCTTACAGCTCTATACGGGGGACGGGGGCTGGAGAGACGACGCG 480
Qy 481 CGTCTGGGGGAGGGCAACTGGGCACTGATGAGCAACAGTGTGAGCGGGGCGGTGCACTG 540
Db 481 CGTCTGGGGGAGGGCAACTGGGCACTGATGAGCAACAGTGTGAGCGGGGCGGTGCACTG 540
Qy 541 GGGGCCCTGTGTAAGTGTGAGGGGCTTTTGTCTAGCAAG 579
Db 541 GGGGCCCTGTGTAAGTGTGAGGGGCTTTTGTCTAGCAAG 579

RESULT 3

US-08-978-523-1
; Sequence 1, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both

TOPOLOGY: both
MOLECULE TYPE: CDNA
US-08-978-523-1

Query Match 93.0%; Score 540.6; DB 2; Length 579;
Best Local Similarity 95.9%; Pred. No. 6,6e-150;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACAGCCCTCTAGTGGCTGACTTTGAGGCTAT 60
DB 1 ATGCCGACCCCAAGCTTCAACCCAGACACAGCCCTCTAGTGGCTGACTTTGAGGCTAT 60
QY 61 AGGCTGAGGAGAAAGGTTATGTCTGTGAGCTGAGGCTGAGGAGGAGGAGGAGGAGGAG 120
DB 61 AGGCTGAGGAGAAAGGTTATGTCTGTGAGCTGAGGCTGAGGAGGAGGAGGAGGAGGAG 120
QY 121 CCGCTGACCAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 121 CCGCTGACCAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 181 TTCTGTACCTGAGCGCTGAGCTACAGTGAACCCAGGCTCAGCCAGCAACGCTTCAAC 240
DB 181 TTCTGTACCTGAGCGCTGAGCTACAGTGAACCCAGGCTCAGCCAGCAACGCTTCAAC 240
QY 241 CAGGTTCCGACGAACTTTTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 241 CAGGTTCCGACGAACTTTTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 301 GTCTTTGGGGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 301 GTCTTTGGGGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 CAAATCCAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 CAAATCCAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 AGTGGCGGCTGGGCGGAGCTTCAAGCTCTATACGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
DB 421 AGTGGCGGCTGGGCGGAGCTTCAAGCTCTATACGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 481 CGTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 481 CGTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 GGGGCGCTGGTAACTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 579
DB 541 GGGGCGCTGGTAACTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 579
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RESULT 4
US-09-949-016-5057
Sequence 5057, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTNER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5057
LENGTH: 582
TYPE: DNA
ORGANISM: Human
US-09-949-016-5057

Query Match 86.2%; Score 501; DB 4; Length 582;
Best Local Similarity 91.4%; Pred. No. 3.4e-138;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACAGCCCTCTAGTGGCTGACTTTGAGGCTAT 60
DB 1 ATGCCGACCCCAAGCTTCAACCCAGACACAGCCCTCTAGTGGCTGACTTTGAGGCTAT 60
QY 61 AGGCTGAGGAGAAAGGTTATGTCTGTGAGCTGAGGCTGAGGAGGAGGAGGAGGAGGAG 120
DB 61 AGGCTGAGGAGAAAGGTTATGTCTGTGAGCTGAGGCTGAGGAGGAGGAGGAGGAGGAG 120
QY 121 CCGCTGACCAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 121 CCGCTGACCAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 181 TTCTGTACCTGAGCGCTGAGCTACAGTGAACCCAGGCTCAGCCAGCAACGCTTCAAC 240
DB 181 TTCTGTACCTGAGCGCTGAGCTACAGTGAACCCAGGCTCAGCCAGCAACGCTTCAAC 240
QY 241 CAGGTTCCGACGAACTTTTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 241 CAGGTTCCGACGAACTTTTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 301 GTCTTTGGGGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 301 GTCTTTGGGGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 CAAATCCAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 CAAATCCAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 AGTGGCGGCTGGGCGGAGCTTCAAGCTCTATACGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
DB 421 AGTGGCGGCTGGGCGGAGCTTCAAGCTCTATACGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 481 CGTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 481 CGTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 GGGGCGCTGGTAACTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 581
DB 541 GGGGCGCTGGTAACTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 581
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RESULT 5
US-09-155-327G-6
Sequence 6, Application US/09155327G
Patent No. 6790637
GENERAL INFORMATION:
APPLICANT: AMRAD Operations Pty Ltd
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
FAMILY OF APOPTOSIS-CONTROLLING GENES
FILE REFERENCE: 2096584
CURRENT APPLICATION NUMBER: US/09/155,327G
CURRENT FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: P89655
PRIOR FILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 583
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(579)
US-09-155-327G-6
Query Match 86.2%; Score 501; DB 4; Length 583;
Best Local Similarity 91.4%; Pred. No. 3.4e-138;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGCCGACCCAGCCCTCAACCCAGACACACCGCCTTATGTCGTAAGCTTAT 60
 Db 1 ATGGGACACCCAGCCCTCGCCGCCAAGACACACGCGCTCTGGGCGAGACTTTGTAGTTAT 60
 QY 61 AGCTGAGGACAGAGGTTATGTCTGTGAGAGTGGGCTGGGGAAGGCGCGCGAC 120
 Db 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGAGTGGGCGCGCGGAGGCGCGAC 120
 QY 121 CCGCTGACACCAAGCAGATGGGCGCTGAGACAGAGTTGAGACCCGTTCCGCGAC 180
 Db 121 CCGCTGACACCAAGCAGATGGGCGCTGAGACAGAGTTGAGACCCGTTCCGCGAC 180
 QY 181 TTCTGTGACCTGGCCGCTCACTGACAGCTGACAGCCAGGCTGAGCCAGCAAGCTTAC 240
 Db 181 TTCTGTGACCTGGCCGCTCACTGACAGCTGACAGCCAGGCTGAGCCAGCAAGCTTAC 240
 QY 241 CAGGTTCCGACGAACTTTTCCAGAGGCGCTTAACTGGGCGCTTGTGGACTTTT 300
 Db 241 CAGGTTCCGACGAACTTTTCCAGAGGCGCTTAACTGGGCGCTTGTGGACTTTT 300
 QY 301 GTCTTTGGGCGCTGCTGTGTGCTGAGAGTGTCAAGAAATGAGACCTTTGGTGGGA 360
 Db 301 GTCTTTGGGCGCTGCTGTGTGCTGAGAGTGTCAAGAAATGAGACCTTTGGTGGGA 360
 QY 361 CAAGTCAAGATTGATGCTGCTGCTGCTGAGAGACAGTCTGCTGAGATCCACAGC 420
 Db 361 CAAGTCAAGATTGATGCTGCTGCTGCTGAGAGACAGTCTGCTGAGATCCACAGC 420
 QY 421 AGTGGCGGCTGGCGGAGCTTCAAGAGCTTAAAGGAGAGGCGGCTTGGAGAGCGAC 480
 Db 421 AGTGGCGGCTGGCGGAGCTTCAAGAGCTTAAAGGAGAGGCGGCTTGGAGAGCGAC 480
 QY 481 CGTCTGCGGAGAGGCACTGCGGATGAGAGACAGTGTGACGAGGCGCTGGACCTG 540
 Db 481 CGTCTGCGGAGAGGCACTGCGGATGAGAGACAGTGTGACGAGGCGCTGGACCTG 540
 QY 541 GGGGCGCTGTAACTGTAGGAGGCTTTTGTCTAGCAAGT 581
 Db 541 GGGGCGCTGTAACTGTAGGAGGCTTTTGTCTAGCAAGT 581

RESULT 6

US-08-798-897-2
 ; Sequence 2, Application US/08798897
 ; Patent No. 5789201
 ; GENERAL INFORMATION:
 ; APPLICANT: Guastella, John
 ; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
 ; NUMBER OF SEQUENCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 New York Avenue, N.W., Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/798,897
 ; FILING DATE: February 11, 1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Esmond, Robert W.
 ; REGISTRATION NUMBER: 32,893
 ; REFERENCE/DOCKET NUMBER: 1483.0140001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 579 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 ; US-08-798-897-2

Query Match 85.6%; Score 497.4; DB 1; Length 579;
 Best Local Similarity 91.2%; Pred. No. 3,9e-137;
 Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 ATGCCGACCCAGCCCTCAACCCAGACACACCGCCTTATGTCGTAAGCTTAT 60
 Db 1 ATGGGACACCCAGCCCTCGCCGCCAAGACACACGCGCTCTGGGCGAGACTTTGTAGTTAT 60
 QY 61 AGCTGAGGACAGAGGTTATGTCTGTGAGAGTGGGCTGGGGAAGGCGCGCGAC 120
 Db 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGAGTGGGCGCGCGGAGGCGCGAC 120
 QY 121 CCGCTGACACCAAGCAGATGGGCGCTGAGACAGAGTTGAGACCCGTTCCGCGAC 180
 Db 121 CCGCTGACACCAAGCAGATGGGCGCTGAGACAGAGTTGAGACCCGTTCCGCGAC 180
 QY 181 TTCTGTGACCTGGCCGCTCACTGACAGCTGACAGCCAGGCTGAGCCAGCAAGCTTAC 240
 Db 181 TTCTGTGACCTGGCCGCTCACTGACAGCTGACAGCCAGGCTGAGCCAGCAAGCTTAC 240
 QY 241 CAGGTTCCGACGAACTTTTCCAGAGGCGCTTAACTGGGCGCTTGTGGACTTTT 300
 Db 241 CAGGTTCCGACGAACTTTTCCAGAGGCGCTTAACTGGGCGCTTGTGGACTTTT 300
 QY 301 GTCTTTGGGCGCTGCTGTGTGCTGAGAGTGTCAAGAAATGAGACCTTTGGTGGGA 360
 Db 301 GTCTTTGGGCGCTGCTGTGTGCTGAGAGTGTCAAGAAATGAGACCTTTGGTGGGA 360
 QY 361 CAAGTCAAGATTGATGCTGCTGCTGCTGAGAGACAGTCTGCTGAGATCCACAGC 420
 Db 361 CAAGTCAAGATTGATGCTGCTGCTGCTGAGAGACAGTCTGCTGAGATCCACAGC 420
 QY 421 AGTGGCGGCTGGCGGAGCTTCAAGAGCTTAAAGGAGAGGCGGCTTGGAGAGCGAC 480
 Db 421 AGTGGCGGCTGGCGGAGCTTCAAGAGCTTAAAGGAGAGGCGGCTTGGAGAGCGAC 480
 QY 481 CGTCTGCGGAGAGGCACTGCGGATGAGAGACAGTGTGACGAGGCGCTGGACCTG 540
 Db 481 CGTCTGCGGAGAGGCACTGCGGATGAGAGACAGTGTGACGAGGCGCTGGACCTG 540
 QY 541 GGGGCGCTGTAACTGTAGGAGGCTTTTGTCTAGCAAG 579
 Db 541 GGGGCGCTGTAACTGTAGGAGGCTTTTGTCTAGCAAG 579

RESULT 7

US-08-978-523-2
 ; Sequence 2, Application US/08978523
 ; Patent No. 5883229
 ; GENERAL INFORMATION:
 ; APPLICANT: Guastella, John
 ; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
 ; NUMBER OF SEQUENCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 New York Avenue, N.W., Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483,0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-978-523-2

Query Match 85.6%; Score 497.4; DB 2; Length 579;
Best Local Similarity 91.2%; Pred. No. 3.9e-137;
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCTTCAACCCGAGACACAGCGCTCTAGTGGTACTTTGAGCTAT 60
DB 1 ATGGCGACCCCAAGCTTCAACCCGAGACACAGCGCTCTAGTGGTACTTTGAGCTAT 60
QY 61 AGGCTGAGGAGAGAGGTTATGTCTGAGAGTGGGCTGGGAGAGGAGCCGAGCCGAC 120
DB 61 AAGCTGAGGAGAGAGGTTATGTCTGAGAGTGGGCTGGGAGAGGAGCCGAGCCGAC 120
QY 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGAGACGATTGAGACCCGCTTCCGCGCACC 180
DB 121 CCACTGACCAAGCCATGCGGGCTGCTGAGAGATGATTGAGACCCGCTTCCGCGCACC 180
QY 181 TTCTTGACCTGGCCGCTCAAGCTACAGTGAACCCAGGCTCAAGCCGCTTCAAC 240
DB 181 TTCTTGATCTGGGCTCAAGCTACAGTGAACCCAGGCTCAAGCCGCTTCAAC 240
QY 241 CAGGTTCCGAGCACTTTTCAAGGGGGCCCTAACTGGGGCCGCTTGGGCAATCTTT 300
DB 241 CAGGTTCCGAGCACTTTTCAAGGGGGCCCTAACTGGGGCCGCTTGGGCAATCTTT 300
QY 301 GTCTTGGGGCTGCGCTGTGTGCTGAGAGTGTCAAGAAATGAGACCTTTGGTGGGA 360
DB 301 GTCTTGGGGCTGCGCTGTGTGCTGAGAGTGTCAAGAAATGAGACCTTTGGTGGGA 360
QY 361 CAGGTCAGAGATTGATCTGAGCTTACCTGAGACAGTCTGGTGAAGTGAATCAAGC 420
DB 361 CAGGTCAGAGATTGATCTGAGCTTACCTGAGACAGTCTGGTGAAGTGAATCAAGC 420
QY 421 AGTGGCGGCTGGGCGAGCTTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGGCGCGG 480
DB 421 AGTGGCGGCTGGGCGAGCTTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGGCGCGG 480
QY 481 CGTCTGCGGAGGAGCACTGCGGCAATGAGTGAAGCACTGTGTGACGGGGCCGTTGCACTG 540
DB 481 CGTCTGCGGAGGAGCACTGCGGCAATGAGTGAAGCACTGTGTGACGGGGCCGTTGCACTG 540
QY 541 GGGGCGCTGTAATGTAAGGGGCTTTTGTGCTAGCAAG 579
DB 541 GGGGCGCTGTAATGTAAGGGGCTTTTGTGCTAGCAAG 579

RESULT 8

US-09-010-147B-23
Sequence 23: Application US/09010147B
Patent No. 6653445
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: Human Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,147B
FILING DATE: 12-NO. 6653445-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 60/034,204
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: P353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURES:
NAME/KEY: CDS
LOCATION: 1..1095
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-010-147B-23

Query Match 62.8%; Score 364.8; DB 4; Length 1098;
Best Local Similarity 90.3%; Pred. No. 8.2e-98;
Matches 390; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCTTCAACCCGAGACACAGCGCTCTAGTGGTACTTTGAGCTAT 60
DB 1 ATGGCGACCCCAAGCTTCAACCCGAGACACAGCGCTCTAGTGGTACTTTGAGCTAT 60
QY 61 AGGCTGAGGAGAGAGGTTATGTCTGAGAGTGGGCTGGGAGAGGAGCCGAGCCGAC 120
DB 61 AAGCTGAGGAGAGAGGTTATGTCTGAGAGTGGGCTGGGAGAGGAGCCGAGCCGAC 120
QY 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGAGACGATTGAGACCCGCTTCCGCGCACC 180
DB 121 CCACTGACCAAGCCATGCGGGCTGCTGAGAGATGATTGAGACCCGCTTCCGCGCACC 180
QY 181 TTCTTGACCTGGCCGCTCAAGCTACAGTGAACCCAGGCTCAAGCCGCTTCAAC 240
DB 181 TTCTTGATCTGGGCTCAAGCTACAGTGAACCCAGGCTCAAGCCGCTTCAAC 240
QY 241 CAGGTTCCGAGCACTTTTCAAGGGGGCCCTAACTGGGGCCGCTTGGGCAATCTTT 300
DB 241 CAGGTTCCGAGCACTTTTCAAGGGGGCCCTAACTGGGGCCGCTTGGGCAATCTTT 300

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-05-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 62.7%; Score 364.4; DB 3; Length 1864;
Best Local Similarity 90.0%; Pred. No. 1.4e-97;
Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCTCAACCCAGACACAGCGGCTGAGTGAAGCTTGTAGGCTAT 60
DB 11 ATGGCGACCCCAAGCTCGGCCCCAGACACAGGAGCTTGTGAGAGCTTGTAGGCTAT 70
QY 61 AGGCTGAGGAGGAAGGTTATGTCGTGAGCTGGGCTGGGAGAGGCCAGCCGCGAC 120
DB 71 AAGCTGAGGAGGAAGGTTATGTCGTGAGCTGGGCTGGGAGAGGCCAGAGCTGAC 130
QY 121 CCGCTGACCAAGCATGCGGCTGCTGAGAGAGGATTGAGACCCGTTTCCGCGAC 180
DB 131 CCGCTGACCAAGCATGCGGCTGCTGAGAGAGGATTGAGACCCGTTTCCGCGAC 190
QY 181 TTCTGACCTGCGGCTGACGTAACAGTACCCAGGCTCAGCCAGCAAGCTTGACC 240
DB 191 TTCTGATCTGGGCTGACGTAAGTACCCAGGCTCAGCCAGCAAGCTTGACC 250
QY 241 CAGGTTCCGACGAACTTTTCAAGGGGCGCTTAAGTGGGCGCTTGTGGCAATCTTT 300
DB 251 CAGGTTCCGACGAACTTTTCAAGGGGCGCTTAAGTGGGCGCTTGTAGCTTTT 310
QY 301 GTCTTTGGGCTGCTGCTGTGTCTGAGAGTGTCAACAAAGATGAGCTTTGTGGA 360
DB 311 GTCTTTGGGCTGCTGCTGTGTCTGAGAGTGTCAACAAAGATGAGATGAGCTGTGGA 370
QY 361 CAAGTCAGAGATGAGATGAGTGTGCTGAGAGACAGCTGTGGCTGAGATGAGTCAAGC 420
DB 371 CAAGTCAGAGATGAGATGAGTGTGCTGAGAGACAGCTGTGGCTGAGATGAGTCAAGC 430
QY 421 AGTGCGGCTGG 432
DB 431 AGTGCGGCTGG 442

RESULT 10
US-09-949-016-16799
Sequence 16799, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16799
LENGTH: 5199
TYPE: DNA
ORGANISM: Human
US-09-949-016-16799

Query Match 62.7%; Score 364.2; DB 4; Length 5199;
Best Local Similarity 90.1%; Pred. No. 2.4e-97;
Matches 390; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCTCAACCCAGACACAGCGGCTTGAAGCTGATCTTGTAGGCTAT 60
DB 2001 ATGGCGACCCCAAGCTCGGCCCCAGACACAGGAGCTTGTGAGAGCTTGTAGGCTAT 2060
QY 61 AGGCTGAGGAGGAAGGTTATGTCGTGAGCTGGGCTGGGAGAGGCCAGCCGCGAC 120
DB 2061 AAGCTGAGGAGGAAGGTTATGTCGTGAGCTGGGCTGGGAGAGGCCAGAGCTGAC 2120
QY 121 CCGCTGACCAAGCATGCGGCTGCTGAGAGAGGATTGAGACCCGTTTCCGCGAC 180

Db 2121 CCACTGACCAACCATGCGGCGAGTGAAGTTCGACCCGCTTCGGGACC 2180
Qy 181 TTCTGACCTGCGCGCTCAGCTGACGACCCCAAGCTCAGCCCAAGCTTCAAC 240
Db 2181 TTCTGATGATGCGCGCTCAGCTGATGATGACCCGAGCTCAGCCCAAGCTTCAAC 240
Qy 241 CAGGTTTCCAGAACTTTTCCAGAGGCGGCGCTTCACTGGGCGGCTTGTGCAATCTTT 2300
Db 2241 CAGGTTTCCAGAACTTTTCCAGAGGCGGCGCTTCACTGGGCGGCTTGTGCAATCTTT 2300
Qy 301 GTCTTTGGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 2301 GTCTTTGGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy 361 CAGTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2300
Db 2361 CAGTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2300
Qy 421 AGTGGCGCTGGG 433
Db 2421 AGTGGCGCTGGG 433

RESULT 11
US-09-949-016-177003
Sequence 177003 Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTNER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CN WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
NUMBER OF SEQ ID NOS: 2000-09-08
SOFTWARE: FASTA/BLAST for Windows Version 4.0
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-177003

Query Match
Best Local Similarity 61.4%; Score 357; DB 4; Length 601;
Matches 381; Conservative 1; Mismatches 41; Indels 0; Gaps 0;
Db 1 ATGCCGACCCCAAGCTTCAACCCCAAGCAAGCTTCTAGTGGCTGACTTTGAGCTAT 60
Qy 179 ATGCCGACCCCAAGCTTCAACCCCAAGCAAGCTTCTAGTGGCTGACTTTGAGCTAT 60
Db 61 AGGCTGAGGCAAGGCTTATGCTGAGAGCTGCGCTGAGGCAAGGCTTCTAGTGGCTAT 238
Qy 239 AGGCTGAGGCAAGGCTTATGCTGAGAGCTGCGCTGAGGCAAGGCTTCTAGTGGCTAT 238
Db 121 CGGCTGACCAAGCAAGCTTCTAGTGGCTGAGGCAAGGCTTCTAGTGGCTAT 120
Qy 299 CGGCTGACCAAGCAAGCTTCTAGTGGCTGAGGCAAGGCTTCTAGTGGCTAT 120
Db 181 TTCTGACCTGCGCGCTCAGCTGACGACCCCAAGCTTCTAGTGGCTAT 298
Qy 359 TTCTGACCTGCGCGCTCAGCTGACGACCCCAAGCTTCTAGTGGCTAT 298
Db 241 CAGGTTTCCAGAACTTTTCCAGAGGCGGCGCTTCACTGGGCGGCTTGTGCAATCTTT 358
Qy 419 CAGGTTTCCAGAACTTTTCCAGAGGCGGCGCTTCACTGGGCGGCTTGTGCAATCTTT 358
Db 301 GTCTTTGGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy 478 GTCTTTGGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478
Db 360 GTCTTTGGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

RESULT 12
US-08-081-448-5
Sequence 5 Application US/08081448
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
NUMBER OF INVENTION: Lawrence H.
CORRESPONDENCE ADDRESSES:
ADDRESS: 321 No. 5646008th Clark Street, Suite 800
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
CURRENT APPLICATION NUMBER: Patent in Release #1.0, Version #1.25
FILING DATE: 19930622
CLASSIFICATION: US/08/081,448
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646008th Clark Street, Suite 800
REGISTRATION NUMBER: 3,268
TELEPHONE: 312-744-0090
TELEFAX: 312-744-0090
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-081-448-5

Query Match
Best Local Similarity 23.2%; Score 134.6; DB 1; Length 926;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
Db 128 ACCAAGCAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
Qy 394 AGCAAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 187
Db 188 ACTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
Qy 454 ACTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
Db 248 CCGAAGCAATTTTCCAGAGGCGGCGCTTCACTGGGCGGCTTGTGCAATCTTT 247
Qy 513 CCGAAGCAATTTTCCAGAGGCGGCGCTTCACTGGGCGGCTTGTGCAATCTTT 247
Db 514 TGATGAACTTCTGCGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 513
Qy 573 TGATGAACTTCTGCGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 573
Db 573 TGATGAACTTCTGCGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 573

QY 308 GGGCTGCTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 367
DB 574 GCGGGGACCTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 633
QY 368 AGATTGATCTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 427
DB 634 CAGCTTGATGAGAGTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 693
QY 428 GCTGGGAGTGTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 487
DB 694 GCTGGGAGTGTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 753
QY 488 GGGAGGAGTGTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 532
DB 754 AGGAGGAGTGTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 798

RESULT 13

US-08-470-670A-6
; Sequence 6, Application US/08470670A
; Patent No. 5834309 5710045
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B. B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD-090-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-470-670A-6

Query Match 23.2%; Score 134.6; DB 2; Length 926;
Best local Similarity 58.3%; Pred. No. 8.8e-30;
Matches 235; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
QY 128 ACCAAGCATGCGGGCTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 187
DB 394 AGCAAGCATGCGGGCTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 453

QY 188 ACTGCGCGCTGAGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 247
DB 454 ACTGCGCGCTGAGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 513
QY 248 CCGAGCACTTTTCAAGGGGCGCTTAACTGGGGCGCTTTGTGGGACAGTCC 307
DB 514 TGAATGAATCTTCCGGGATGGGGTAAACTGGGGCGCTTTGTGGGACAGTCC 573
QY 308 GGGCTGCTGTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 367
DB 574 GCGGGGACCTGTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 633
QY 368 AGATTGATCTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 427
DB 634 CAGCTTGATGAGAGTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 693
QY 428 GCTGGGAGTGTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 487
DB 694 GCTGGGAGTGTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 753
QY 488 GGGAGGAGTGTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 532
DB 754 AGGAGGAGTGTGTGTGTGAGAGTGTCAACAAAGATGAGACCTTTGTGGGACAGTCC 798

RESULT 14

US-08-481-739-1
; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,739
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,518
; FILING DATE: 04-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Deconci, Giulio A. (GAD)
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RPI-034CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 742-4214
; TELEFAX: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-481-739-1

Query Match 23.2%; Score 134.6; DB 3; Length 926;
Best local Similarity 58.3%; Pred. No. 8.8e-30;

Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCTGTGAGACGAGTTTGAGACCCGTTTCCGCGCACTTCTCTG 187
 Db 394 AGCAAGCCCTGAGGAGGAGGAGCGAGGTTTGAATGCGGTACCGCGGCAATTCAGTG 453
 QY 188 ACCTGGCCCTGACGTACAGGTGACCCAGGCTCAGCCAGCAAGCTTCAACCGAGTTT 247
 Db 454 ACTGACATCCAGCTCCACATCAACCCAGGAGCAGCATTCAGAGCTTTGAAACAGTAA 513
 QY 248 CCGAGCACTTTTCCAGAGGGGCGCTTAATGAGGCGCTTCTTGTGCACTTTTCTCTTG 307
 Db 514 TGAATGAATCTTTCCGAGATGAGTAACTGGGGTCCCATTTGCTTCTCTCTG 573
 QY 308 GGGCTGCTGTGTGTGAGAGTGTCAACAAGAAATGAGCCCTTGTGTGGAGCAAGTCC 367
 Db 574 GCGGGGCACTGTGTGTGAAAGGTGACAGAGAGATGCAAGTATTTGTGAGTGGATG 633
 QY 368 AGGATTTGATCTGTGCTTACCTTGAGACACGCTTGTGCTGATCCACAGCAGTGGG 427
 Db 634 CAGCTTGGATGGCCACTTACCTGAAATGACCACTAGAGCTTGTGATCCAGAGAAAGGG 693
 QY 428 GCTGGGCGGACTTCAAGCTCTTAACGGGAGCGGGGCGCTTGAGAGACGACGCGCTTGC 487
 Db 694 GCTGGGATCTTTTGTGAACTCTATGGAACTATGGAACTAGCAGCGCGGAAAGGGCC 753
 QY 488 GGGAGGGCACTGGGCAATGATGAGCAAGTGTGTGACGGGGGCGG 532
 Db 754 AGGAACGCTTCAACCGCTGTGCTCTGACGGGCAATGACTGTGGCG 798

RESULT 15

US-09-167-921-1
 ; Sequence 1, Application US/09167921A
 ; Patent No. 6172216
 ; GENERAL INFORMATION:
 ; APPLICANT: Benmelt, C. Frank
 ; APPLICANT: Dean, Nicholas M.
 ; APPLICANT: Monia, Brett P.
 ; APPLICANT: Nickoloff, Brian J.
 ; APPLICANT: Zhang, Qingsong
 ; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
 ; FILE REFERENCE: ISPH-0324
 ; CURRENT APPLICATION NUMBER: US/09/167,921A
 ; CURRENT FILING DATE: 1998-10-07
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 926
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (135)..(836)
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: L20121 Genbank
 ; DATABASE ENTRY DATE: 1994-07-26
 ; US-09-167-921-1

Query Match 23.2%; Score 134.6; DB 3; Length 926;
 Best Local Similarity 58.3%; Pred. No. 8.8e-30;
 Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCTGTGAGACGAGTTTGAGACCCGTTTCCGCGCACTTCTCTG 187
 Db 394 AGCAAGCCCTGAGGAGGAGGAGCGAGGTTTGAATGCGGTACCGCGGCAATTCAGTG 453
 QY 188 ACCTGGCCCTGACGTACAGGTGACCCAGGCTCAGCCAGCAAGCTTCAACCGAGTTT 247
 Db 454 ACTGACATCCAGCTCCACATCAACCCAGGAGCAGCATTCAGAGCTTTGAAACAGTAA 513
 QY 248 CCGAGCACTTTTCCAGAGGGGCGCTTAATGAGGCGCTTCTTGTGCACTTTTCTCTTG 307

Db 514 TGAATGAATCTTTCCGAGATGAGGTAACGTGGGTCCGATTTGCGCTTTTCTCTTCG 573
 QY 308 GGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAAATGAGCCCTTGTGTGGAGCAAGTCC 367
 Db 574 GCGGGGCACTGTGTGTGAAAGGTGACAGAGAGATGCAAGTATTTGTGAGTGGATG 633
 QY 368 AGGATTTGATCTGTGCTTACCTTGAGACAGTGTGTGCTGATGATCCACAGCAGTGGG 427
 Db 634 CAGCTTGGATGGCCACTTACCTGAAATGACCACTAGAGCTTGTGATCCAGAGAAAGGG 693
 QY 428 GCTGGGCGGACTTCAAGCTCTTAACGGGAGCGGGGCGCTTGAGAGACGACGCGCTTGC 487
 Db 694 GCTGGGATCTTTTGTGAACTCTATGGAACTATGGAACTAGCAGCGCGGAAAGGGCC 753
 QY 488 GGGAGGGCACTGGGCAATGATGAGCAAGTGTGTGACGGGGGCGG 532
 Db 754 AGGAACGCTTCAACCGCTGTGCTCTGACGGGCAATGACTGTGGCG 798

Search completed: April 10, 2005, 20:17:22
 Job time : 144.753 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 18:38:08 ; Search time 498.642 Seconds
(without alignments)
7060.905 Million cell updates/sec

Title: US-09-925-674B-8

Perfect score: 581
Sequence: 1 atgcgcagcccccagctcctaac.....gcctttttctagcaagtc 581

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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- 3: /cgn2_6/ptodata/1/pubpna/US06_PCT_NEW_PUB.seq:*
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- 19: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
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| 1 | 563.4 | 97.0 | 582 9 US-09-925-674A-8 | Sequence 8, Appl1 |
| 2 | 505.8 | 87.1 | 582 18 US-10-384-339C-37 | Sequence 37, Appl1 |
| 3 | 505.8 | 87.1 | 583 9 US-09-925-674A-6 | Sequence 6, Appl1 |
| 4 | 501 | 86.2 | 582 19 US-10-479-832A-4 | Sequence 4, Appl1 |
| 5 | 364.4 | 62.7 | 1864 10 US-09-809-391-130 | Sequence 130, App |
| 6 | 364.4 | 62.7 | 1864 10 US-09-882-171-130 | Sequence 130, App |
| 7 | 364.4 | 62.7 | 1864 17 US-10-164-861-130 | Sequence 130, App |
| 8 | 364.2 | 62.7 | 578 16 US-10-029-386-10549 | Sequence 10549, A |
| 9 | 363.2 | 62.5 | 433 16 US-10-029-386-24249 | Sequence 24249, A |
| 10 | 212.2 | 36.5 | 6049 15 US-10-311-455-201 | Sequence 201, App |
| 11 | 191 | 32.9 | 6049 15 US-10-311-455-202 | Sequence 202, App |

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|----|-------|------|----------------------------|--------------------|
| 12 | 140.4 | 24.2 | 660 17 US-10-402-017-9 | Sequence 9, Appl1 |
| 13 | 139.6 | 24.0 | 540 17 US-10-402-017-5 | Sequence 5, Appl1 |
| 14 | 139.4 | 24.0 | 600 17 US-10-402-017-7 | Sequence 7, Appl1 |
| 15 | 138.8 | 23.9 | 151 16 US-10-029-386-27084 | Sequence 27084, A |
| 16 | 138.8 | 23.9 | 590 16 US-10-029-386-13384 | Sequence 13384, A |
| 17 | 137.8 | 23.7 | 530 16 US-09-864-761-17690 | Sequence 17690, A |
| 18 | 134.6 | 23.2 | 636 16 US-10-169-223-13 | Sequence 13, Appl1 |
| 19 | 134.6 | 23.2 | 660 17 US-10-402-017-11 | Sequence 11, Appl1 |
| 20 | 134.6 | 23.2 | 702 17 US-09-959-987-9 | Sequence 9, Appl1 |
| 21 | 134.6 | 23.2 | 863 17 US-10-402-017-3 | Sequence 3, Appl1 |
| 22 | 134.6 | 23.2 | 926 9 US-09-734-846-1 | Sequence 1, Appl1 |
| 23 | 134.6 | 23.2 | 926 9 US-09-734-847A-39 | Sequence 39, Appl1 |
| 24 | 134.6 | 23.2 | 926 9 US-09-952-278-5 | Sequence 5, Appl1 |
| 25 | 134.6 | 23.2 | 926 15 US-10-072-830-3 | Sequence 3, Appl1 |
| 26 | 134.6 | 23.2 | 926 16 US-10-302-262-1 | Sequence 1, Appl1 |
| 27 | 134.6 | 23.2 | 926 17 US-10-402-017-1 | Sequence 1, Appl1 |
| 28 | 134.6 | 23.2 | 926 17 US-10-641-643-1430 | Sequence 1430, Ap |
| 29 | 134.6 | 23.2 | 926 18 US-10-717-597-87 | Sequence 87, Appl1 |
| 30 | 134.6 | 23.2 | 926 18 US-10-776-827-106 | Sequence 106, App |
| 31 | 134.6 | 23.2 | 926 18 US-10-825-282-47 | Sequence 47, Appl1 |
| 32 | 134.6 | 23.2 | 926 19 US-10-479-832A-3 | Sequence 3, Appl1 |
| 33 | 134.6 | 23.2 | 1236 18 US-10-792-517-1 | Sequence 1, Appl1 |
| 34 | 130.6 | 22.5 | 1455 18 US-10-792-517-7 | Sequence 7, Appl1 |
| 35 | 126.8 | 21.8 | 600 9 US-09-864-761-7360 | Sequence 7360, Ap |
| 36 | 126.6 | 21.8 | 1466 18 US-10-283-975A-394 | Sequence 394, App |
| 37 | 126.4 | 21.8 | 720 17 US-10-148-953A-8 | Sequence 8, Appl1 |
| 38 | 125.8 | 21.7 | 555 9 US-09-918-995-33305 | Sequence 33305, A |
| 39 | 125.8 | 21.7 | 555 9 US-09-864-761-24081 | Sequence 24081, A |
| 40 | 125.8 | 21.7 | 555 9 US-10-029-386-20790 | Sequence 20790, A |
| 41 | 125 | 21.5 | 717 16 US-10-053-645A-20 | Sequence 20, Appl1 |
| 42 | 125 | 21.5 | 720 17 US-10-148-953A-6 | Sequence 6, Appl1 |
| 43 | 125 | 21.5 | 720 17 US-10-148-953A-7 | Sequence 7, Appl1 |
| 44 | 125 | 21.5 | 720 17 US-10-297-321-1 | Sequence 1, Appl1 |
| 45 | 125 | 21.5 | 720 18 US-10-770-668-17 | Sequence 17, Appl1 |

ALIGNMENTS

RESULT 1
US-09-925-674A-8
Sequence 8, Application US/09925674A
Patent No. US20020119943A1
GENERAL INFORMATION:
APPLICANT: AMRAD Operations Pty Ltd
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-1, BELONGS TO THE bcl-2
FILE REFERENCE: 11686a
CURRENT APPLICATION NUMBER: US/09/925,674A
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/925,674
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: P8965
PRIOR FILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 8
LENGTH: 582
TYPE: DNA
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(579)
US-09-925-674A-8

Query Match 97.0%; Score 563.4; DB 9; Length 582;
Best Local Similarity 98.1%; Pred. No. 2,9e-160;
Matches 570; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATCCGACCCGACCTTCAACCCGACACACGCGCTCTAGCTGACTTGTAGCTAT 60
DB 1 ATGCGACCCGACCTTCAACCCGACACACGCGGCTCTAGCTGACTTGTAGCTAT 60

| | | | |
|----|-----|--|-----|
| QY | 61 | AGCGTAGAGGAGAAAGGGTTATGTCGTGAGACTGGGCTGGGGAAGGCCACAGCCGCCAG | 120 |
| Db | 61 | AGCGTAGAGGAGAAAGGGTTATGTCGTGAGACTGGGCTGGGGAAGGCCACAGCCGCCAG | 120 |
| QY | 121 | CCGCTGCACCAAGCCATGCGGGGCTGCTGAGAGCAAGTTTAGACCCTTTTCCGCGCAAC | 180 |
| Db | 121 | CCGCTGCACCAAGCCATGCGGGGCTGCTGAGAGCAAGTTTAGACCCTTTTCCGCGCAAC | 180 |
| QY | 181 | TTCTCTGACCTGGGCGGCTCAGCTACAGTGACCCCAAGGCTAGGCCCAAGCGTTCAAC | 240 |
| Db | 181 | TTCTCTGACCTGGGCGGCTCAGCTACAGTGACCCCAAGGCTAGGCCCAAGCGTTCAAC | 240 |
| QY | 241 | CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGTCTTTGAGCAATCTTT | 300 |
| Db | 241 | CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGTCTTTGAGCAATCTTT | 300 |
| QY | 301 | GTCCTTTGGGGGTGCGCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAAGCTTTTGATGGA | 360 |
| Db | 301 | GTCCTTTGGGGGTGCGCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAAGCTTTTGATGGA | 360 |
| QY | 361 | CAAGTCCAGAGATTGATGCTGCGCTTACCTGAGACAAGTCTGCTGACTGAGTCCACAGC | 420 |
| Db | 361 | CAAGTCCAGAGATTGATGCTGCGCTTACCTGAGACAAGTCTGCTGACTGAGTCCACAGC | 420 |
| QY | 421 | AGTGGCGGCTGGGGGGGACCTTACAGAGCTCTAAGCGGGGACGGGGGCTCTGAGAGAGCGACGG | 480 |
| Db | 421 | AGTGGCGGCTGGGGGGGACCTTACAGAGCTCTAAGCGGGGACGGGGGCTCTGAGAGAGCGACGG | 480 |
| QY | 481 | CGTCTGCGGGAGGGCAACTGGGCAATGAGTAGACAACAGTGTGACGGGGGCCGTGGCACTG | 540 |
| Db | 481 | CGTCTGCGGGAGGGCAACTGGGCAATGAGTAGACAACAGTGTGACGGGGGCCGTGGCACTG | 540 |
| QY | 541 | GGGGCCCTGGTAACGTAGAGGGGCCCTTTTTCCTAGCAAGTG | 581 |
| Db | 541 | GGGGCCCTGGTAACGTAGAGGGGCCCTTTTTCCTAGCAAGTG | 581 |

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RESULT 2
US-10-384-339C-37
; Sequence 37, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzler, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: bcl-2
; PATENT DOCUMENT NUMBER: US9747
US-10-384-339C-37

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| Query Match | 87.1%; | Score 505.8; | DB 18; | Length 582; |
| Best Local Similarity | 91.9%; | Pred. No. 7.8e-143; | | |
| Matches 534; | Conservative 0; | Mismatches 47; | Indels 0; | Gaps 0 |
| 1 ATGCGGACCCGCTCAACCCGACACACGCGCTCTGATGAGTACCTTTGTAGGCTAT 60 | | | | |

| | | | |
|----|-----|---|-----|
| Db | 1 | ATGGCAGACCCGACGCTCGGCCCCAGACACAAGGGGCTCTGGGTGGCAGACTTGTGAAGTTAT | 60 |
| Oy | 61 | AGGCTGAGGCGAAGGGTTATGTCTGTGAGAGCTGGGCTGGGGAGAGGCCAGCGCGGAC | 120 |
| Db | 61 | AAAGCTAGGCGAAGGGTTATGTCTGTGAGAGCTGGGCTGGGGAGAGGCCAGAGAGCTGAC | 120 |
| Oy | 121 | CCGCTGCACCAAGCCATGCGGGCTGCTGAGACGAGTTTGAAGCCGTTTTCCGCGGACC | 180 |
| Db | 121 | CGGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTTCGAGACCGGCTTCCGGCGACC | 180 |
| Oy | 181 | TTTCTGACCTGGCGGCTGACGTAAACGTGACCCAGGCTTCAAGGCCAGCAAGCTTAC | 240 |
| Db | 181 | TTTCTGAACTGGCGGCTGACGTATGACCCAGGCTGACCCAGCAAGCGTTTACC | 240 |
| Oy | 241 | CAGTTTCCGAGCAACTTTTCAAGGGGGCCCTAACTGGGCGCTTGTGTGCAATTCCTT | 300 |
| Db | 241 | CAGGTCCTCGAGCAACTTTTCAAGGGGGCCCAACTGGGCGGCTTGTGAGCTTCTTT | 300 |
| Oy | 301 | GTCTTTGGGGCTGCGCCCTGTGTCTGAGAGTGTCAAACAAGAAATGAGACCTTTGTGGGA | 360 |
| Db | 301 | GTCTTTGGGGCTGCACTGTGTCTGAGAGTGTCAAACAAGAGATGAGAACCACTGTGTGGGA | 360 |
| Oy | 361 | CAAGTCCAGAAATTTGATCGTGGCCTAACCTGGAGACAGCTGGCTGACTGGATCCAGC | 420 |
| Db | 361 | CAAGTCCAGAGATGATGTGGCTTAACCTGGAGACAGCGGCTGGCTGACTGGATCCAGC | 420 |
| Oy | 421 | AGTGGGCGCTGGGCGGACTTCAACAGCTTATACGGGGAACGGGGCCCTGAGAGACGACGG | 480 |
| Db | 421 | AGTGGGGGCTGGGCGGAGTTCAACACTTATACGGGGAACGGGGCCCTGAGAGAGCGCGG | 480 |
| Oy | 481 | CGTCTGCGGAGGGGCAACTGGGCATGAGTGAACACAGTGTGAACGGGGGCGCTGGCACTG | 540 |
| Db | 481 | CGTCTCGGGAAGGGAACTGGGCATCAGTGAAGAACAGTGTGAACGGGGGCGTGGCACTG | 540 |
| Oy | 541 | GGGGCCCTGGTAACTGTAGGGGCTTTTGTGTAGCAAGT | 581 |
| Db | 541 | GGGGCCCTGGTAACTGTAGGGGCTTTTGTGTAGCAAGT | 581 |

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RESULT 3
US-09-925-674A-6
; Sequence 6, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-1, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686A
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 583
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-925-674A-6

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| | | | | | | | | | | |
|-------|------------|--|--------------|-------|--------------|----|--------|--------|------|---|
| Query | Match | Similarity | 87.1% | Score | 505.8 | DB | 9 | Length | 583 | |
| | Best local | Similarity | 91.9% | Pred. | No. 7,8e-143 | | | | | |
| | Matches | 534 | Conservative | 0 | Mismatches | 47 | Indels | 0 | Gaps | 0 |
| QY | 1 | ATGCCAGACCCAGGCTCAACCCAGACACAGGCGCTCAAGGCGCATTTGTAGGCTAT | 60 | | | | | | | |
| Db | 1 | ATGGGAGCCCCAGGCTCGGCCCCAGACACAGGCGCTCTGGCGCAGATTTGTAACTTAT | 60 | | | | | | | |


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QY 61 AGGCTGAGGCGAAGGGTTATGTCGTGAGAGTGGGCGCTGGGGGAAGGCCAGCCGCGAC 120
DB 61 AAGCTGAGGCGAAGGGTTATGTCGTGAGAGTGGGCGCTGGGGGAAGGCCAGCGCTGAC 120
QY 121 CCGCTGACCAAGGCAATGCGGGCTGCTGAGACGAGTTTGAGACCCGTTTCCGCGCAC 180
DB 121 CCGCTGACCAAGGCAATGCGGGCAAGCTGGAGATGAGTTGAGACCCGTTTCCGCGCAC 180
QY 181 TTCTCTGACCTGGCCGCTCAGCTTACAGTGAACCCAGGCTCAGCCAGCAAGCCTTAC 240
DB 181 TTCTCTGACCTGGCCGCTCAGCTTACAGTGAACCCAGGCTCAGCCAGCAAGCCTTAC 240
QY 241 CAGGTTTCCGAGCACTTTTCCAGAGGGGGCCCTAATGCGGGCCGCTTGTGAGCAATCTT 300
DB 241 CAGGTTTCCGAGCACTTTTCCAGAGGGGGCCCTAATGCGGGCCGCTTGTGAGCAATCTT 300
QY 301 GTCTTTGGGGGCTGCGCTGTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTTGGTGG 360
DB 301 GTCTTTGGGGGCTGCGCTGTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTTGGTGG 360
QY 361 CAAGTCAGAGATTGATGCTGCTTACCTGAGACAGCTTGGCTGACTGATCCACAGC 420
DB 361 CAAGTCAGAGATTGATGCTGCTTACCTGAGACAGCTTGGCTGACTGATCCACAGC 420
QY 421 AGTGGCGGCTGGGGGCACTTCAAGCTCTATACGGGGGACGGGGCCCTGGAGAGACGAC 480
DB 421 AGTGGCGGCTGGGGGCACTTCAAGCTCTATACGGGGGACGGGGCCCTGGAGAGACGAC 480
QY 481 CGTTCGCGGAGGCGCAACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540
DB 481 CGTTCGCGGAGGCGCAACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540
QY 541 GGGGCCCTGTGTAAGTGAAGGAGGCTTTTGTCTAGCAAGTG 581
DB 541 GGGGCCCTGTGTAAGTGAAGGAGGCTTTTGTCTAGCAAGTG 581
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RESULT 4
US-10-479-832A-4
; Sequence 4, Application US/10479832A
; Publication No. US20050064407A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson Research Pty Ltd
; TITLE OF INVENTION: Bcl-2 DNasezymes
; FILE REFERENCE: WJ13107942
; CURRENT APPLICATION NUMBER: US/10/479, 832A
; CURRENT FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-832A-4
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Query Match 86.2%; Score 501; DB 19; Length 582;
Best Local Similarity 91.4%; Pred. No. 2,2e-141;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1 ATGCCGACCCCAAGCTTCAACCCGACACACAGGCGCTCTAGAGTGAATTTGTAGGCTAT 60
DB 1 ATGCCGACCCCAAGCTTCAACCCGACACACAGGCGCTCTAGAGTGAATTTGTAGGCTAT 60
QY 61 AGGCTGAGGCGAAGGGTTATGTCGTGAGAGTGGGCGCTGGGGGAAGGCCAGCCGCGAC 120
DB 61 AAGCTGAGGCGAAGGGTTATGTCGTGAGAGTGGGCGCTGGGGGAAGGCCAGCGCTGAC 120
QY 121 CCGCTGACCAAGGCAATGCGGGCTGCTGAGACGAGTTTGAGACCCGTTTCCGCGCAC 180
DB 121 CCGCTGACCAAGGCAATGCGGGCAAGCTGGAGATGAGTTGAGACCCGTTTCCGCGCAC 180
QY 181 TTCTCTGACCTGGCCGCTCAGCTTACAGTGAACCCAGGCTCAGCCAGCAAGCCTTAC 240
DB 181 TTCTCTGACCTGGCCGCTCAGCTTACAGTGAACCCAGGCTCAGCCAGCAAGCCTTAC 240
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DB 181 TTCTCTATCTGGGGCTCAGCTGATGTGATGCCAGAGCTCAGCCAAACGCTTAC 240
QY 241 CAGGTTTCCGAGCACTTTTCCAGAGGGGGCCCTAATGCGGGCCGCTTGTGAGCAATCTT 300
DB 241 CAGGTTTCCGAGCACTTTTCCAGAGGGGGCCCTAATGCGGGCCGCTTGTGAGCAATCTT 300
QY 301 GTCTTTGGGGGCTGCGCTGTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTTGGTGG 360
DB 301 GTCTTTGGGGGCTGCGCTGTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTTGGTGG 360
QY 361 CAAGTCAGAGATTGATGCTGCTTACCTGAGACAGCTTGGCTGACTGATCCACAGC 420
DB 361 CAAGTCAGAGATTGATGCTGCTTACCTGAGACAGCTTGGCTGACTGATCCACAGC 420
QY 421 AGTGGCGGCTGGGGGCACTTCAAGCTCTATACGGGGGACGGGGCCCTGGAGAGACGAC 480
DB 421 AGTGGCGGCTGGGGGCACTTCAAGCTCTATACGGGGGACGGGGCCCTGGAGAGACGAC 480
QY 481 CGTTCGCGGAGGCGCAACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540
DB 481 CGTTCGCGGAGGCGCAACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540
QY 541 GGGGCCCTGTGTAAGTGAAGGAGGCTTTTGTCTAGCAAGTG 581
DB 541 GGGGCCCTGTGTAAGTGAAGGAGGCTTTTGTCTAGCAAGTG 581
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RESULT 5
US-09-809-391-130
; Sequence 130, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1648)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-130
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Query Match 62.7%; Score 364.4; DB 10; Length 1864;
Best Local Similarity 90.0%; Pred. No. 5.4e-100;
Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;
QY 1 ATGCCGACCCCAAGCTTCAACCCGACACACAGGCGCTCTAGAGTGAATTTGTAGGCTAT 60
DB 11 ATGCCGACCCCAAGCTTCAACCCGACACACAGGCGCTCTAGAGTGAATTTGTAGGCTAT 70
QY 61 AGGCTGAGGCGAAGGGTTATGTCGTGAGAGTGGGCGCTGGGGGAAGGCCAGCCGCGAC 120
DB 71 AAGCTGAGGCGAAGGGTTATGTCGTGAGAGTGGGCGCTGGGGGAAGGCCAGCGCTGAC 130
QY 121 CCGCTGACCAAGGCAATGCGGGCTGCTGAGACGAGTTTGAGACCCGTTTCCGCGCAC 180
DB 131 CCGCTGACCAAGGCAATGCGGGCAGCKGAGATGATGATGAGACCCGCTTCCGCGCAC 190
QY 181 TTCTCTGACCTGGCCGCTCAGCTTACAGTGAACCCAGGCTCAGCCAGCAAGCCTTAC 240
DB 191 TTCTCTGACCTGGCCGCTCAGCTTACAGTGAACCCAGGCTCAGCCAGCAAGCCTTAC 250
QY 241 CAGGTTTCCGAGCACTTTTCCAGAGGGGGCCCTAATGCGGGCCGCTTGTGAGCAATCTT 300
DB 241 CAGGTTTCCGAGCACTTTTCCAGAGGGGGCCCTAATGCGGGCCGCTTGTGAGCAATCTT 300
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Db 251 CAGGTCGATGAATTTCCTTCAAGGGGCCCACTGGGGCCGCTGTGACCTTCTTT 310
 Qy 301 GTCTTTGGGGGCTGCTGTGTGTGTGTGAGTGTCAACAAAGAAATGAGCTTTGGTGGGA 360
 Db 311 GTCTTTGGGGGCTGCTGTGTGTGTGTGAGTGTCAACAAAGAAATGAGCACTGGTGGGA 370
 Qy 361 CAAATCCAGATTTGATCTGCTTACCTGAGACACGCTTGGCTGATGATCCACAGC 420
 Db 371 CAAATCCAGATTTGATGTTGCTTACCTGAGACACGCTTGGCTGATGATCCACAGC 430
 Qy 421 AGTGGGGGCTGG 432
 Db 431 AGTGGGGGCTGG 442

RESULT 6
 US-09-882-171-130

/ Sequence 130, Application US/09882171
 / Publication No. US20030175858A1
 / GENERAL INFORMATION:

/ APPLICANT: Ruben et al.

/ TITLE OF INVENTION: 186 Human Secreted proteins
 / FILE REFERENCE: P2002P2

/ CURRENT FILING DATE: 2001-06-18
 / PRIOR FILING DATE: 2001-03-16

/ PRIOR APPLICATION NUMBER: 09/809,391
 / PRIOR FILING DATE: 1998-09-08

/ PRIOR APPLICATION NUMBER: 09/149,476
 / PRIOR FILING DATE: 1998-03-06

/ PRIOR APPLICATION NUMBER: PCT/US98/04493
 / PRIOR FILING DATE: 1997-03-07

/ PRIOR APPLICATION NUMBER: 60/040,162
 / PRIOR FILING DATE: 1997-03-07

/ PRIOR APPLICATION NUMBER: 60/040,333
 / PRIOR FILING DATE: 1997-03-07

/ PRIOR APPLICATION NUMBER: 60/038,621
 / PRIOR FILING DATE: 1997-03-07

/ PRIOR APPLICATION NUMBER: 60/040,626
 / PRIOR FILING DATE: 1997-03-07

/ PRIOR APPLICATION NUMBER: 60/040,334
 / PRIOR FILING DATE: 1997-03-07

/ PRIOR APPLICATION NUMBER: 60/040,336
 / PRIOR FILING DATE: 1997-03-07

/ PRIOR APPLICATION NUMBER: 60/040,163
 / PRIOR FILING DATE: 1997-03-07

/ PRIOR APPLICATION NUMBER: 60/047,600
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,615
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,597
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,502
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,633
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,583
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,617
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,618
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,503
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,592
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,581
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,584
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,500
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/047,587
 / PRIOR FILING DATE: 1997-05-23

/ PRIOR APPLICATION NUMBER: 60/056,911
 / PRIOR FILING DATE: 1997-08-22

/ PRIOR APPLICATION NUMBER: 60/047,492
 / PRIOR FILING DATE: 1997-05-23
 / PRIOR APPLICATION NUMBER: 60/047,598
 / PRIOR FILING DATE: 1997-05-23
 / PRIOR APPLICATION NUMBER: 60/047,613
 / PRIOR FILING DATE: 1997-05-23
 / PRIOR APPLICATION NUMBER: 60/047,582
 / PRIOR FILING DATE: 1997-05-23
 / PRIOR APPLICATION NUMBER: 60/047,596
 / PRIOR FILING DATE: 1997-05-23
 / PRIOR APPLICATION NUMBER: 60/047,612
 / PRIOR FILING DATE: 1997-05-23
 / PRIOR APPLICATION NUMBER: 60/047,632
 / PRIOR FILING DATE: 1997-05-23
 / PRIOR APPLICATION NUMBER: 60/047,601
 / PRIOR FILING DATE: 1997-05-23
 / PRIOR APPLICATION NUMBER: 60/043,580
 / PRIOR FILING DATE: 1997-04-11
 / PRIOR APPLICATION NUMBER: 60/043,568
 / PRIOR FILING DATE: 1997-04-11
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 / PRIOR FILING DATE: 1997-04-11
 / PRIOR APPLICATION NUMBER: 60/043,569
 / PRIOR FILING DATE: 1997-04-11
 / PRIOR APPLICATION NUMBER: 60/043,311
 / PRIOR FILING DATE: 1997-04-11
 / PRIOR APPLICATION NUMBER: 60/043,671
 / PRIOR FILING DATE: 1997-04-11
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 / PRIOR APPLICATION NUMBER: 60/043,312
 / PRIOR FILING DATE: 1997-04-11
 / PRIOR APPLICATION NUMBER: 60/043,313
 / PRIOR FILING DATE: 1997-04-11
 / PRIOR APPLICATION NUMBER: 60/043,672
 / PRIOR FILING DATE: 1997-04-11
 / PRIOR APPLICATION NUMBER: 60/043,315
 / PRIOR FILING DATE: 1997-04-11
 / PRIOR APPLICATION NUMBER: 60/048,974
 / PRIOR FILING DATE: 1997-06-06
 / PRIOR APPLICATION NUMBER: 60/056,886
 / PRIOR FILING DATE: 1997-08-22
 / PRIOR APPLICATION NUMBER: 60/056,877
 / PRIOR FILING DATE: 1997-08-22
 / PRIOR APPLICATION NUMBER: 60/056,889
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 / PRIOR APPLICATION NUMBER: 60/056,872
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 / PRIOR APPLICATION NUMBER: 60/056,882
 / PRIOR FILING DATE: 1997-08-22
 / PRIOR APPLICATION NUMBER: 60/056,637
 / PRIOR FILING DATE: 1997-08-22
 / PRIOR APPLICATION NUMBER: 60/056,903
 / PRIOR FILING DATE: 1997-08-22
 / PRIOR APPLICATION NUMBER: 60/056,888
 / PRIOR FILING DATE: 1997-08-22
 / PRIOR APPLICATION NUMBER: 60/056,879
 / PRIOR FILING DATE: 1997-08-22
 / PRIOR APPLICATION NUMBER: 60/056,880
 / PRIOR FILING DATE: 1997-08-22
 / PRIOR APPLICATION NUMBER: 60/056,894
 / PRIOR FILING DATE: 1997-08-22

| | Best Local Similarity | 90.0% | Pred. No. 5.4e-100; | Matches 389; | Conservative 1; | Mismatches 42; | Indels 0; | Gaps 0 |
|--|-----------------------|--|---------------------|--------------|-----------------|----------------|-----------|--------|
| QY | 1 | ATGCCGACCCCAAGCCTTCAACCCAGACACACGCGCTCTTAGTGGCTGACTTTGTAGGCTAT | 60 | | | | | |
| DB | 11 | ATGGGCAACCCCAAGCCTCGGCCCCAGACACACGCGCTCTGGTGGCAGACTTTGTAGGTTAT | 70 | | | | | |
| QY | 61 | AGCGTGAGGCAAGAGGGTTATGTCTGTGGAGCTGGGCGCTGGGAAAGGCCACGCCGAC | 120 | | | | | |
| DB | 71 | AAGCTGAGGCAAGAGGGTTATGTCTGTGGAGCTGGGCGCTGGGAAAGGCCACGACGTGAC | 130 | | | | | |
| QY | 121 | CCGCTGACCAACAAGCCATCGGGCTCTGGAGACGAGTTTGAAGCCGTTTCGCCGCGAC | 180 | | | | | |
| DB | 131 | CCGCTGACCAACAAGCCATCGGGCGACGCKGAGATGAGTTTGAGACCCGCTTCGGCGCAC | 190 | | | | | |
| QY | 181 | TTCTCTGACCTGGCGCGCTCAAGTACACGTGACCCCAAGGCTCAGCCGACGACGCTTAC | 240 | | | | | |
| DB | 191 | TTCTCTGATCTGGCGGCTCAAGTATGACCCCAAGGCTCAGCCCAACAAGCTTAC | 250 | | | | | |
| QY | 241 | CAGGTTTCCGACGAATCTTTCCAAAGGGGGCCCTTACCTGGGCGCTTGTGGCACTTCTT | 300 | | | | | |
| DB | 251 | CAGGCTTCCGATGAATCTTTTCAAGGGGGCCCAACTGGGGCGCGCTGTAGCTTCTT | 310 | | | | | |
| QY | 301 | GTCCTTGGGGGCTGCGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGGCTTTGGTGGA | 360 | | | | | |
| DB | 311 | GTCCTTGGGGGCTGCACTGTGTGTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA | 370 | | | | | |
| QY | 361 | CAAGTCCAGATTGGATGTTGGGCTTACCTGAGACACGTCTGGCTGACTGATTCACAGC | 420 | | | | | |
| DB | 371 | CAAGTCAAGAGTGGATGTTGGGCTTACCTGAGAGACGGGCTGGCTGACTGATTCACAGC | 430 | | | | | |
| QY | 421 | AGTGGCGGCTGG 432 | | | | | | |
| DB | 431 | AGTGGGCGCTGG 442 | | | | | | |
| RESULT 7 | | | | | | | | |
| US-10-164-861-130 | | | | | | | | |
| ; Sequence 130; Application US/10164861 | | | | | | | | |
| ; Publication No. US20030225248A1 | | | | | | | | |
| ; GENERAL INFORMATION: | | | | | | | | |
| ; APPLICANT: Rosen et al. | | | | | | | | |
| ; TITLE OF INVENTION: 186 Human Secreted proteins | | | | | | | | |
| ; FILE REFERENCE: P2002P1 | | | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/10/164,861 | | | | | | | | |
| ; CURRENT FILING DATE: 2002-06-10 | | | | | | | | |
| ; PRIOR APPLICATION NUMBER: US/09/149,476 | | | | | | | | |
| ; PRIOR FILING DATE: 1998-09-08 | | | | | | | | |
| ; PRIOR APPLICATION NUMBER: PCT/US98/04493 | | | | | | | | |
| ; PRIOR FILING DATE: 1998-03-06 | | | | | | | | |
| ; NUMBER OF SEQ ID NOS: 757 | | | | | | | | |
| ; SOFTWARE: PatentIn Ver. 2.0 | | | | | | | | |
| ; SEQ ID NO 130 | | | | | | | | |
| ; LENGTH: 1864 | | | | | | | | |
| ; TYPE: DNA | | | | | | | | |
| ; ORGANISM: Homo sapiens | | | | | | | | |
| ; FEATURE: | | | | | | | | |
| ; NAME/KEY: SITE | | | | | | | | |
| ; LOCATION: (1648) | | | | | | | | |
| ; OTHER INFORMATION: n equals a,t,g, or c | | | | | | | | |
| US-10-164-861-130 | | | | | | | | |
| Query Match 62.7%; Score 364.4; DB 17; Length 1864; | | | | | | | | |
| Best Local Similarity 90.0%; Pred. No. 5.4e-100; | | | | | | | | |
| Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps | | | | | | | | |

QY 121 CCGCTGACCAAGCCATGCGGCTGCTGAGACGAGTTTGAACCCGTTTCCGCGCAC 180
 DB 131 CCGCTGACCAAGCCATGCGGCTGCTGAGACGAGTTTGAACCCGTTTCCGCGCAC 180
 QY 181 TTCTCTGATCTGCGGCTGCTGAGACGAGTTTGAACCCGTTTCCGCGCAC 190
 DB 191 TTCTCTGATCTGCGGCTGCTGAGACGAGTTTGAACCCGTTTCCGCGCAC 190
 QY 241 CAGGTTTCCGAGAACTTTTCCAGGGGCGCTTCACTGAGCCCAAGCCCTTCCAC 240
 DB 251 CAGGTTTCCGAGAACTTTTCCAGGGGCGCTTCACTGAGCCCAAGCCCTTCCAC 240
 QY 301 GCTTTGGGGCTGCGCTGCTGAGAGTGTCAAGAAAGAGAGCTTTTGGTGGGA 360
 DB 311 GCTTTGGGGCTGCGCTGCTGAGAGTGTCAAGAAAGAGAGCTTTTGGTGGGA 360
 QY 361 CAGGTTTCCGAGAACTTTTCCAGGGGCGCTTCACTGAGCCCAAGCCCTTCCAC 240
 DB 371 CAGGTTTCCGAGAACTTTTCCAGGGGCGCTTCACTGAGCCCAAGCCCTTCCAC 240
 QY 421 AGTGGCGGCTGG 432
 DB 431 AGTGGCGGCTGG 442

RESULT 8
 US-10-029-386-10549
 / Sequence 10549
 / Publication No. US20030194704A1
 / GENERAL INFORMATION:
 / APPLICANT: Penn, Sharon G.
 / APPLICANT: Hamel, David R.
 / TITLE OF INVENTION: HUMAN G.
 / FILE OF INVENTION: EXPRESSION ANALYSIS TWO
 / CURRENT APPLICATION NUMBER: US/10/029,386
 / NUMBER OF SEQ ID NOS: 34288
 / SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 / SEQ ID NO 10549
 / LENGTH: 578
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / OTHER INFORMATION: MAP TO CH14.3
 / OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 4.2
 / OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 3.3
 / OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
 / OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
 / OTHER INFORMATION: EST HUMAN HIT: AL157512.1, EVALUATE 0.00e+00
 / OTHER INFORMATION: EST HUMAN HIT: AL157512.1, EVALUATE 0.00e+00
 / OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALUATE 2.00e-72

Query Match
 Best Local Similarity 62.7%; Score 364.2; DB 16; Length 578;
 Matches 390; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
 QY 1 ATGCCGACCCGCTCAACCCGACACACAGCCCTTCTAGTGGCTTCTTGTGAGTTT 60
 DB 105 ATGCCGACCCGCTCAACCCGACACACAGCCCTTCTAGTGGCTTCTTGTGAGTTT 60
 QY 61 AGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGGCTTGTGAGCTTGTGAGTTT 164
 DB 165 AGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGGCTTGTGAGCTTGTGAGTTT 164
 QY 121 CCGCTGACCAAGCCATGCGGCTGCTGAGACGAGTTTGAACCCGTTTCCGCGCAC 180
 DB 225 CCGCTGACCAAGCCATGCGGCTGCTGAGACGAGTTTGAACCCGTTTCCGCGCAC 180

QY 181 TTCTCTGATCTGCGGCTGCTGAGACGAGTTTGAACCCGTTTCCGCGCAC 190
 DB 285 TTCTCTGATCTGCGGCTGCTGAGACGAGTTTGAACCCGTTTCCGCGCAC 190
 QY 241 CAGGTTTCCGAGAACTTTTCCAGGGGCGCTTCACTGAGCCCAAGCCCTTCCAC 240
 DB 345 CAGGTTTCCGAGAACTTTTCCAGGGGCGCTTCACTGAGCCCAAGCCCTTCCAC 240
 QY 301 GCTTTGGGGCTGCGCTGCTGAGAGTGTCAAGAAAGAGAGCTTTTGGTGGGA 360
 DB 405 GCTTTGGGGCTGCGCTGCTGAGAGTGTCAAGAAAGAGAGCTTTTGGTGGGA 360
 QY 361 CAGGTTTCCGAGAACTTTTCCAGGGGCGCTTCACTGAGCCCAAGCCCTTCCAC 240
 DB 465 CAGGTTTCCGAGAACTTTTCCAGGGGCGCTTCACTGAGCCCAAGCCCTTCCAC 240
 QY 421 AGTGGCGGCTGG 433
 DB 525 AGTGGCGGCTGG 537

RESULT 9
 US-10-029-386-24249
 / Sequence 24249
 / Publication No. US20030194704A1
 / GENERAL INFORMATION:
 / APPLICANT: Penn, Sharon G.
 / APPLICANT: Hamel, David R.
 / TITLE OF INVENTION: HUMAN G.
 / FILE OF INVENTION: EXPRESSION ANALYSIS TWO
 / CURRENT APPLICATION NUMBER: US/10/029,386
 / NUMBER OF SEQ ID NOS: 34288
 / SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 / SEQ ID NO 24249
 / LENGTH: 433
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / OTHER INFORMATION: MAP TO CH14.3
 / OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 4.2
 / OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 3.3
 / OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
 / OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
 / OTHER INFORMATION: EST HUMAN HIT: AL157512.1, EVALUATE 0.00e+00
 / OTHER INFORMATION: EST HUMAN HIT: AL157512.1, EVALUATE 0.00e+00
 / OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALUATE 2.00e-72

Query Match
 Best Local Similarity 62.5%; Score 363.2; DB 16; Length 433;
 Matches 389; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
 QY 1 ATGCCGACCCGCTCAACCCGACACACAGCCCTTCTAGTGGCTTCTTGTGAGTTT 60
 DB 2 ATGCCGACCCGCTCAACCCGACACACAGCCCTTCTAGTGGCTTCTTGTGAGTTT 60
 QY 61 AGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGGCTTGTGAGCTTGTGAGTTT 164
 DB 62 AGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGGCTTGTGAGCTTGTGAGTTT 164
 QY 121 CCGCTGACCAAGCCATGCGGCTGCTGAGACGAGTTTGAACCCGTTTCCGCGCAC 180
 DB 122 CCGCTGACCAAGCCATGCGGCTGCTGAGACGAGTTTGAACCCGTTTCCGCGCAC 180
 QY 181 TTCTCTGATCTGCGGCTGCTGAGACGAGTTTGAACCCGTTTCCGCGCAC 190
 DB 182 TTCTCTGATCTGCGGCTGCTGAGACGAGTTTGAACCCGTTTCCGCGCAC 190

| | | | | | |
|----|-----|----------------|-------------------------|----------------------------|---------------|
| QY | 241 | CAGATTCCGACGA | CTTTTCCAGGGGGCCCTTA | CTGAGGCGCGTCTGAGCAATCTTT | 300 |
| Db | 242 | CAGGCTCCGATGAA | CTTTTTCAAGGGGGCCCA | CTGAGGCGCGCTTGAACCTTTT | 301 |
| QY | 301 | GTCCTTGGGGCTG | CCCTGTGTGCTGAGATGTCA | CAAAAGAAATGAGCCCTTTGTGTGGA | 360 |
| Db | 302 | GTCCTTGGGGCTG | CACTGTGTGTGTGAGATGTCA | CAAGAGATGAAACA | CTGTGTGGA 361 |
| QY | 361 | CAAGTCCAGAGATT | GATCGTGGCTTACCTGAGAGACA | CGTCTGGGCTGACTGGAATCCACAGC | 420 |
| Db | 362 | CAAGTCCAGAGATG | ATGTGTGGCTTACCTGAGAGACG | CAGCTGGCTGACTGGAATCCACAGC | 421 |
| QY | 421 | AGTGGCGGCTGG | 432 | | |
| Db | 422 | AGTGGGGGCTGG | 433 | | |

```

RESULT 10
US-10-311-455-201
Sequence 201, Application US/10311455
Publication No. US20030143606a1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311.455
CURRENT FILING DATE: 2002-12-16
PRIORITY APPLICATION NUMBER: PCT/EP01/07537
PRIORITY FILING DATE: 2001-07-02
PRIORITY APPLICATION NUMBER: DE 10032529.7
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: DE 10043826.1
PRIORITY FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 201
LENGTH: 6049
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-201

```

| Query Match | Best Local Similarity | Score | 21.2 -2; | DB 15; | Length 6049; |
|-------------|-----------------------|--|----------|-----------------|--------------|
| Matches | 295; | Conservative | 0; | Mismatches 133; | Indels 0; |
| | | | | Gaps | 0; |
| QY | 1 | ATGCGACCCAGCCTCAACCCAGACACACGCGCTAGTGGCTGACTTTGTAGCTAT | 60 | | |
| Db | 5001 | ATGCGCATTTTAGTTTCGGTTTAGATATACGGGGTTTGGTGGTAGATTTTGTAGTTAT | 5060 | | |
| QY | 61 | AGCGTAGGCGAAGGGTATGTCTGTGAGCTGGGCTCGGGGAAAGGCCACCGCGAC | 120 | | |
| Db | 5061 | AAGTTGAGGTGAAAGGGTTATGTTGTGCAAGTGGTTTCGGGGAAGGTTTGTAGTTAT | 5120 | | |
| QY | 121 | CCGCTGCACCAAGGCATGCGGGGCTGTGAGACGAGTTTGAAACCGTTTCGGCGGCAC | 180 | | |
| Db | 5121 | TCGTTGTATTAAGTTATATCGGGGTACTTGGAGATGAGTTTCGAGATTCGTTTCGGCGCTAT | 5180 | | |
| QY | 181 | TTCTCTGACCTGGCGGCTCAGCTACACGTGACCCAGGCTCAGGCCAGCAACGCTTCACC | 240 | | |
| Db | 5181 | TTTTTTGATTTGGGGGTTTAGTGTATGTGATTTTAGGTTTAGTTATTAACGTTTTAT | 5240 | | |
| QY | 241 | CAGGTTTCGACGAACCTTTCCAAAGGGGACCCTAACTGGGGCGCTTGTGTGCAATCTTT | 300 | | |
| Db | 5241 | TAGGTTTTCGATGAAATTTTTTAAAGGGGGTTTTAATTTGGGGCGCTTTGTGTGTTTTTT | 5300 | | |
| QY | 301 | GTCCTTTGGGGGTCGCCCTGTGTGTGACAGTGTCAACAAGAAATGACACCTTTGGTGGGA | 360 | | |
| Db | 5301 | GTTTTTGGGGTGTATGTGTGTGTGATGAGGTGTAAATTAAGAGATGGAATTAATGTGTGGGA | 5360 | | |

| | | | |
|----|------|---|------|
| Oy | 361 | CAAAATCAGGATTGGATCGTGCCTACCTGAGACAGTCGTGGCTGATCGATCAAGC | 420 |
| Db | 5361 | TAACTGTAGGAGTGATGCTGTTTAATTGGAGACGTAGTTGGTTGATTTGATTAATGT | 5420 |
| Oy | 421 | AGTGGCCGCCCTGGC | 433 |
| Db | 5421 | AGTGGGGGTTGGG | 5433 |

```

US-10-311-455-202/c
; RESULT 11
; Sequence 202, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Expression of Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 202
; LENGTH: 6049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-202

```

| Query Match | Similarity | Score | DB | Length |
|-------------|------------|-------------------|----|-----------------------------------|
| Best Local | 55.7% | Pred. No. 1.8e-47 | | |
| Matches | 278; | Conservative | 0; | Mismatches 145; Indels 0; Gaps 0; |

| Query | 1 | ATGCGACGCCAGCGCTCAACCCCGAGACACAGCGCGCTAGTGGCTGACTTTGTAGGCTAT | 60 |
|-------|------|--|-----|
| Db | 1049 | ATTAACGACCCCAACTCTGACCCCAACACAGAACTTAATTAACAACTTTATTAATATAT | 990 |
| Query | 61 | AGGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGGCGTGGGGAAGGCCAGCGCGGAC | 120 |
| Db | 989 | AAACTTAACAAAAAATTAATATCTAATAAACTAACCCCGAAAAAACCAACAATTAAC | 930 |
| Query | 121 | CCGCTGCACCAAGCGCATGCGGGCGCTGCGAGACGAGTTTGTAGACCGCTTTCCGCGCAC | 180 |
| Db | 929 | CCGCTAACCAAAACCATACGAAACAACCTTAAATTAATTCGAAACCCGCTCCGAGCAC | 870 |
| Query | 181 | TTCTCTACCGTGGCGGCTCAGCTTACAGTGAACGCGCCAGGCTCAGGCCGACGACGTTACC | 240 |
| Db | 869 | TTCTCTAATCTAACGACTCAACTACATATTAACCCCAACCTTAAACCAACAACGTTTACC | 810 |
| Query | 241 | CAGGTTTCCGACGAACTTTTCCAAAGGGGGGCGCTTAAGTGGGCGCTTTGTGTGCAATCTTT | 300 |
| Db | 809 | CAAACTCTCCGATTAACCTTTTCAAAAAABAAACCCCAACTTAAACCGCTTTATTAACCTTTT | 750 |
| Query | 301 | GTCCTTTGGGGCGTGGCGCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGGGA | 360 |
| Db | 749 | ATCTTTTAAACTACACTATATTACTTAATAAATATCAACAAAAAATTAACCACTAATAAAA | 690 |
| Query | 361 | CAAGTCCAGATTTGGAATCGTGGCGCTTACTGTGAGACACAGTCTGGGTGACTGATTCACAGC | 420 |
| Db | 689 | CAAAATACAAAAAATTAATTAATTAACCTACTTAAAAACGAACTTAATTAATTAATTCACAAC | 630 |
| Query | 421 | AGT 423 | |
| Db | 629 | AAT 627 | |

RESULT 12

```
US-10-402-017-9
; Sequence 9, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENBERGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; TITLE OF INVENTION: such cells
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del16-83)
US-10-402-017-9
```

```
Query Match          24.2%; Score 140.4; DB 17; Length 660;
Best Local Similarity 57.5%; Pred. No. 2.8e-32;
Matches 252; Conservative 0; Mismatches 186; Indels 0; Gaps 0;
```

```
QY 95 GGCCTGGGGAAGCCGACCCGACCCGCTGACCAAGCCATGCGGGCTGCTGAGACG 154
DB 185 GCCCGCGGTACGCGCCGACAGACGACGCTAAAGCAAGCCCTGAGAGAGCCGCGCATG 244
QY 155 AGTTGAGACCCGTTTCCGCGCACTTCTGACCTGCGCGCTCAGTACAGTACC 214
DB 245 AGTTGAGCTGCGGTACCGCGCGGCTTCACTGATCAACATCCAGCTTCAATTAACCC 304
QY 215 CAGGCTCAGCCCAAGCGCTTCAACCCAGTTTCCGACGAACTTTCCAAAGGGGCCCTTA 274
DB 305 CAGGAGCTGCAATCAAGCTTTGAACAGAGTGAATGAATCTTCCGGATGGGGTAA 364
QY 275 ACTGGGCGCTTCTTGTGCGATCTTTTGTCTTGTGGGCGCTGCGTGTGCTGAGAGTCA 334
DB 365 ACTGGGCGCTGATGTTGGCTTTTCTTCTTCTTGGTGGAGCCCTGATGTGGAAGCGTAG 424
QY 335 ACAAGAATGAGCCCTTGTGTGGAGCAAGTCCAGATGTGATGTGGCTTACTTGAAGA 394
DB 425 ACAAGAGATGCAAGTATGTGTGATCGATCGAAGTTGATGCCAATCACTTGAATG 484
QY 395 CACGCTGCTGACTGATGATCCAGACAGTGGCGGCTGGGCGGACTTCAAGCTTATACG 454
DB 485 ACACACCTAGAGCCCTTGTGATCCAGAGCAACGGCGCTGGGACACTTGTGGAACCTTAG 544
QY 455 GGGAGCGGGCCCTTGAAGAGCGACGCGCTTCTGCGAGAGGGCAACTGGGCACTGAGTGA 514
DB 545 GAAACAATGCGACGCTGAGAGCGGAAAGGCCAGAGAGCGCTTCAACCGCTGTTCTGA 604
QY 515 CAGTGTGACGGGGGGCGG 532
DB 605 CGGGCAATGACTGTGCGTG 622
```

RESULT 13

```
US-10-402-017-5
; Sequence 5, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENBERGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; TITLE OF INVENTION: such cells
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; CURRENT FILING DATE: 2003-03-28
```

```
;; PRIOR APPLICATION NUMBER: US 60/369,307
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 5
;; LENGTH: 540
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del126-83)
US-10-402-017-5
```

```
Query Match          24.0%; Score 139.6; DB 17; Length 540;
Best Local Similarity 56.7%; Pred. No. 4.8e-32;
Matches 287; Conservative 0; Mismatches 204; Indels 15; Gaps 1;
```

```
QY 27 CACACGCGCTCTAGTGGCTGACTTTGTAGGCTATAGGCTGAGGACAGAGGTTATGTTG 86
DB 12 CAACCGGAGCTAGTGTGATCTTCTCTCAAGCTTCCCAAGAAAGATACAGCTG 71
QY 87 TGAAGCTGGGCGCTGGGGAAGCCGCGCCGACCCGCTGACCAAGCCATGCGGCTGC 146
DB 72 GAGTGGG-----CCGACGACGACCGCTAAAGCAAGCGCTGAGAGAGC 116
QY 147 TGAGACGAGTTTGAAGACCCGTTTCCGCGCACTTCTGACCTGCGCGCTGAGCTACA 206
DB 117 CGCGAGATGATTTGAGCTGTGGTACCGCGGGGCTTCAAGTATCAATCCAGCTTCA 176
QY 207 CTGACCCCAAGGCTCAGCCCAAGCAAGCTTCAACCAAGTTTCCGACGAACTTTCCAAG 266
DB 177 TATTAACCCCGAGGACTGATATCAAAAGCTTTGAACAGTGAATGAATCTTCCGGGA 236
QY 267 GGGCCCTTAAGTGGGCGCTTGTGGCAATCTTGTCTTTGGGCGCGCTGTGCTGA 326
DB 237 TGGGTTAACTGGGGTGCATGTGGCTTTTCTTCTTCTTGGGAGCCCTGTGTGA 296
QY 327 GAGTGTCAACAAAGAAATGAGGCTTGTGTGGACAAGTCCAGATGTGATCTGTGCTTA 386
DB 297 AAGGTAGACAAAGAGATGAGGTATTTGTGATCGGATCGCAAGTTGATGGCCACTTA 356
QY 387 CTGAGACACGCTGTGCTGATGATCCACAGACAGTGGCGGCTGGGCGGACTTCAAGC 446
DB 357 CCGTAATGACCAACTTGAAGCTTGTGATCCAGGCAACAGCGGCGCTGGGACACTTCTGTGA 416
QY 447 TCTAATCGGGGAGGGGCGCTTGAAGAGCGACGCGGCTGTGGGAGGGGCAACTGGGCA 506
DB 417 ACTTACGGAACAAATGACAGCACTGAGAGCGGAAAGGCCAGAGCGCTTCAACCGCTG 476
QY 507 AGTAGCACAGTGTGACGCGGGGCGG 532
DB 477 GTTCCGTGAGCGGCGATGACTGTGCTG 502
```

RESULT 14

```
US-10-402-017-7
; Sequence 7, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENBERGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; TITLE OF INVENTION: such cells
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del46-83)
US-10-402-017-7

Query Match 24.0%; Score 139.4; DB 17; Length 600;
Best Local Similarity 57.1%; Pred. No. 5.6e-32;
Matches 254; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

QY 88 GGAAGCTGGGCGCTGGGGAAGGCGCCGAGCCGCGAGCCGCGACCAAGCCATGCGGCGTCT 147
DB 118 GGAAGCTGAATCAGAGAGGCGCGCCGAGCCGCGAGCCGCGATTAAGCAAGCGCTAGAGAGGCC 177
QY 148 GGAAGCAGATTGAGACCCGCTTCCGCGCACTTCTCTGACCTGCGCGCTCAGCTACAC 207
DB 178 GGCATGATGTTGAGCTGCGGCTACCGGCGGCGGCTTCAAGTATCAATCCAGCTTCAT 237
QY 208 GTGACCCCAAGGCTCAGCCAGCAAGCTTCAACCGATTTCCAGAACTTTCCAGAGG 267
DB 238 ATTAACCCAGGAGTGCATATCAAGCTTTGAAACAGATGAAATGAATCTTCCGGGAT 297
QY 268 GGCCTTAAGTGGGCGGCTTCTTGTGAGCAATCTTGTGAGGCGCTGAGTGTAG 327
DB 298 GGGGTAACTGGGCTCGCATTTGCGCTTTTCTTCTTCTGAGCCCTCTGTGTGAA 357
QY 328 AGTGTCAACAAGAAATGAGCCCTTGTGTGAGCAAGTCCAGATTGATGTCGCTAC 387
DB 358 AGGCTAGACAGAGAGATGAGGATGTTGTGATGAGATCGCAATTGGATGCCACCTAC 417
QY 388 CTGAGACACAGCTCTGCTGACTGATCCACAGCAGTGGCGGCTGGCGGCACTTCAAGCT 447
DB 418 CTGATATACCACTTAGAGCCCTTGTGATCAGAGCAACGCGCGCTGGACACTTCTGTGAA 477
QY 448 CTATACGGGGGAGCGGCGCTTGTGAGAGCAGCGGCTGCGGGAGGGCAACTGGGCATGA 507
DB 478 CTCTACGAAACAAATGACAGCTGAGAGCCGGAAGGCCAGAGCGCTTCAACCGCTGG 537
QY 508 GTGAGCACAGTGTGACGCGGCGCG 532
DB 538 TTCCTGACGGGCACTGATGCTGCTG 562

RESULT 15

US-10-029-386-27084
; Sequence 27084, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27084
; LENGTH: 151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 5.00e-70
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11
; OTHER INFORMATION: NT HIT: g14574571, EVALUE 9.00e-80
US-10-029-386-27084

Query Match 23.9%; Score 138.8; DB 16; Length 151;
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DB 61 GCGGAACTGGGCACTGATGAGACAGATGAGTGAAGCGGGGCGGCTGCACTGGGGGCGCTGCT 120
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DB 121 AACTGTAGGGGCGCTTTTGTCTAGCAAGTG 150

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| Db | 121 | CCGCTGCACCAAGCCATGGGGGTGTGTGAGAGCACTTTGAGACCGGTTTCCGCGCAC | 180 |
| QY | 181 | TTCTCTGACCTGGCGGCTCAGCTACACGTGACCCGAGGCTCAGCCAGCAACGCTTCACC | 240 |
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| Db | 421 | AGTGGCGGCTGGGCGGAGTTTCAACAGCTCTTAACGGGGACGGGGCCTTGAGAGAGGCACGG | 480 |
| QY | 481 | CGTCTGCCGGAAGGCACTGGGCAATGATGAGACACAGTGTGACGGGGGCGGTGGCACTG | 540 |
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| | |
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| ACCESSION | Mus musculus adult male testis cDNA, RIKEN full-length enriched |
| VERSION | library, clone:493048BD08 product:Bc12-1like 2, full insert |
| KEYWORDS | sequence. |
| SOURCE | AKO15644 |
| ORGANISM | AKO15644.1 GI:12854052 |
| REFERENCE | HMC, CAP trapper. |
| AUTHORS | Mus musculus (house mouse) |
| TITLE | Mus musculus |
| JOURNAL | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| MEDLINE | Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. |
| PUBMED | 1 |
| REFERENCE | Carninci, P. and Hayashizaki, Y. |
| AUTHORS | High-efficiency full-length cDNA cloning |
| TITLE | Mech. Enzymol. 303, 19-44 (1999) |
| JOURNAL | 99279253 |
| MEDLINE | 10349636 |
| PUBMED | 2 |
| REFERENCE | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., |
| AUTHORS | Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. |
| TITLE | Normalization and subtraction of cap-trapper-selected cDNAs to |
| JOURNAL | prepare full-length cDNA libraries for rapid discovery of new genes |
| MEDLINE | Genome Res. 10 (10), 1617-1630 (2000) |
| PUBMED | 11042159 |
| REFERENCE | 3 |
| AUTHORS | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., |

| | |
|-----------|---|
| TITLE | Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer |
| JOURNAL | Genome Res. 10 (11), 1757-1771 (2000) |
| PUBMED | 20530913 |
| REFERENCE | 11076861 |
| AUTHORS | 4 |
| TITLE | The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. |
| JOURNAL | Functional annotation of a full-length mouse cDNA collection |
| REFERENCE | Nature 409, 685-690 (2001) |
| AUTHORS | 5 |
| TITLE | The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. |
| JOURNAL | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs |
| REFERENCE | Nature 420, 563-573 (2002) |
| AUTHORS | 6 (bases 1 to 1949) |
| TITLE | Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukushima,Y., Funumoto,M., Hanagasaki,T., Hara,A., Hayasaka,N., Hiramoto,K., Hiraoaka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukabe,T., Kato,H., Kawai,J., Koike,Y., Konno,H., Konda,M., Koysa,S., Kurihara,C., Matsumiya,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Saeki,D., Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Sogabe,Y., Suetsuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toyota,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) |
| COMMENT | Please visit our web site (http://genome.gsc.riken.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GGAAGAAGAAAGATCCAAAGCTCTTTTATTATTATTA 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GGAGAGCAATTCGTGAGTTAATTAAATTAATGCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size compressed longer than 7 kb was selected before cloning. Vector: a modified plasmidscript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI, 3' end: BamBI. Host: DHIOB. Location/Qualifiers 1..1949 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:493048BD08" /db_xref="taxon:10090" /clone="493048BD08" /sex="male" /tissue_type="testis" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 132..713 /note="unnamed protein product; Bcl2-like 2 (MGD GI:108052) putative" /codon_start=1 /protein_id="BA229912.1" /db_xref="GI:12854053" |
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| SOURCE | |
| CDS | |

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 LOCUS Mus musculus adult male lung cDNA, RIKEN full-length enriched
 DEFINITION library, clone:1200009L24 product:Bcl2-like 2, full insert
 sequence.

ACCESSION AK004680
 VERSION AK004680.1 GI:12836027
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE Genome Res. 10 (10), 1617-1630 (2000)
 PUBMED 20499374
 11042159

REFERENCE
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, Y., Nishi, K., Kitesuna, T., Tashiro, H., Itoh, M.,
 Sumi, N., Iehi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861

REFERENCE
 4 The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5

REFERENCE
 5 The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3487)

JOURNAL
 AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
 Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
 Hiraoaka, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Izawa, M.,
 Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M.,
 Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
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 Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
 Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
 Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
 Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
 Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission

TITLE Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of
 JOURNAL Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
 url:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216)

COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further
 details.

CDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5' GAGAGAGAGAGCGCGGCACTCGAGTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse transcriptase
 and subsequently enriched for full-length by cap-trapper. Second
 strand cDNA was prepared with the primer adapter of sequence [5'
 GAGAGAGAGAGCAAGGCTCAATTAATTAATTAACCCGCCCC 3']. cDNA was
 cleaved with XhoI and ScaI. Cloning sites, 5' end: ScaI; 3' end:
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FEATURES
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ORIGIN
Query Match 96.4%; Score 560.2; DB 3; Length 3487;
Best Local Similarity 97.8%; Pred. No. 4,3e-134;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 ATGCCGACCCCGCTCAACCCAGACACGCGCTTAGTGGCTGACTTTGTAGCTTAT 60
DB 209 ATGGGACCCCGCTCAACCCAGACACGCGCTTAGTGGCTGACTTTGTAGCTTAT 268
QY 61 AGGCTGAGGACGAAGGGTATGTCTGTGAGAGCTGGGCTTGGGGAAGGCCCGCCGAC 120
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RESULT 4
LOCUS BY715200 969 bp mRNA linear EST 17-DEC-2002
DEFINITION BY715200 RIKEN full-length enriched, adult male testis Mus musculus
cDNA clone 493048BD08 5', mRNA sequence.
ACCESSION BY715200
VERSION BY715200.1 GI:27128317
KEYWORDS EST.

SOURCE
ORGANISM Mus musculus (house mouse)
REFERENCE
AUTHORS Mus musculus
Okazaki, Y., Furuno, M., Kanukawa, T., Adachi, J., Bono, H., Kondo, S.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schombach, C., Gojopori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanpin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Bruscia, V.,
Ciothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragan, T. A.,
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Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
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Sandelin, A., Schneider, C., Sempke, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Vardaro, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wymshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayashizu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arikawa, T., Fukuda, S., Hara, A., Haseizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shingawa, A., Yasuniishi, A., Yoshino, Y., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
JOURNAL MEDLINE
PUBMED
COMMENT
TITLE
Contact: Yoshihide Hayashizaki:
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P.,
Fukuda, S., Haseizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
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Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submision
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
source Location/Qualifiers
1..969


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QY 420 CAGT-GGCGCTGGGCGGAGCTTACAGCTCTATACCGGAGAC-GGGGCCCTGGAGACGCA 477
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RESULT 6
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LOCUS Homo sapiens BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY421020
VERSION AY421020.1 GI:39776977
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 582)
AUTHORS Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 582)
AUTHORS Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submision
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them
based on alignment.
FEATURES
location/Qualifiers
source 1..582
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>582
/gene="BCL2L2"
/locus_tag="HCM7418"
gene
ORIGIN
Query Match 86.2%; Score 501; DB 9; Length 582;
Best Local Similarity 91.4%; Pred. No. 7e-119;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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QY 241 CAGGTTCCAGCAACTTTTCCAAAGGGGCCCTTAAGTGGGCCGTCTTGTGGCAATCTTT 300
DB 241 CAGGTTCCAGCAACTTTTCCAAAGGGGCCCTTAAGTGGGCCGTCTTGTGGCAATCTTT 300
QY 301 GTCTTTGGGGGCTGGCCTGTGTGCTGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
DB 301 GTCTTTGGGGGCTGACGTGTGTGCTGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
QY 361 CAACTCAGAGATTGATCGTGGCTTACCTGGAACAAGTGTGCTGACTGATCAAGC 420
DB 361 CAACTCAGAGATTGATCGTGGCTTACCTGGAACAAGTGTGCTGACTGATCAAGC 420
QY 421 AGTGGGGGCTGGGGGAGCTTACAGCTCTATACCGGAGACCGGGGCCCTGGAGAGACGACG 480
DB 421 AGTGGGGGCTGGGGGAGCTTACAGCTCTATACCGGAGACCGGGGCCCTGGAGAGAGCGCG 480
QY 481 CGTCTCGGAGAGGAGCACTGGGATGATGAGACAGTGGTGGAGGGGGCCGTGGCACTG 540
DB 481 CGTCTCGGAGAGGAGCACTGGGATGATGAGACAGTGGTGGAGGGGGCCGTGGCACTG 540
QY 541 GGGGCCCTGTGTAAGTGAAGGCGCTTTTGTCTGCAAGTG 581
DB 541 GGGGCCCTGTGTAAGTGAAGGCGCTTTTGTCTGCAAGTG 581

RESULT 7
CD617893/c 727 bp mRNA linear EST 12-JAN-2004
LOCUS 5605747501 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD617893
ACCESSION CD617893
VERSION CD617893.1 GI:40266158
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 727)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
location/Qualifiers
source 1..727
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1lb="FLP"
/Note="Vector: pDrive Cloning Vector"
ORIGIN
Query Match 86.2%; Score 501; DB 6; Length 727;
Best Local Similarity 91.4%; Pred. No. 7.2e-119;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Db 428 TTCTGTATCTGGGGCTCAGCTGATGTGACCCAGGCTCAGCCCAACAAAGCTTCACC 369
Qy 241 CAGGTTTCCAGCAACTTTTCCAAAGGGGGCCCTTAACTGGGGCCGTCTTGTGGCACTTCTT 300
Db 368 CAGGTTTCCAGCAACTTTTCCAAAGGGGGCCCTTAACTGGGGCCGTCTTGTGGCACTTCTT 309
Qy 301 GTCTTTGGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGGGA 360
Db 308 GTCTTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAAGAAATGAGAACTGTGGGA 249
Qy 361 CAACTCCAGAGTTGGATCGTGGCCCTTACTGGAGACAGCTGTGGCTGATGTGATCCACAGC 420
Db 248 CAACTGCAAGAGTGGATGTGTGGCTTACTGGAGACAGCGGCTGTGCTGATGTGATCCACAGC 189
Qy 421 AGTGGCGGCTGGCGGCACTTCAACAGCTCTATACGGGGAACGGGGCCCTTGAAGAGCGACGG 480
Db 188 AGTGGGGGCTGGCGGAGTTTCAAGCTCTATACGGGGAACGGGGCCCTTGAAGAGCGCGG 129
Qy 481 CGTCTGCGGAGGGCACTGGGCACTGAGTGAACAAGTGTGACGGGGGCGGTGGCACTG 540
Db 128 CGTCTGCGGAGGGGAACCTGGGCACTGAGTGAACAAGTGTGACGGGGGCGGTGGCACTG 69
Qy 541 GGGGCCCTGTGTAAGTGTGAGGGCCCTTTTGTCTAGCAAGTG 581
Db 68 GGGGCATCTGTAACTGTAGGGGCCCTTTTGTCTAGCAAGTG 28

RESULT 8

CD617891/c 629 bp mRNA linear EST 12-JAN-2004

LOCUS CD617891 F1P Homo sapiens cDNA, mRNA sequence.

DEFINITION CD617891

ACCESSION CD617891.1 GI:40266156

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 629)

AUTHORS Fu, G.R., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.

TITLE Circular rapid amplification of cDNA ends for high-throughput

extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)

CONTACT: Fu GK

INCYTE Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

TEL: 6508454102

EMAIL: gfu@incyte.com.

LOCATION/Qualifiers

1. 629

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_id="F1P"

/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 86.0%; Score 499.4; DB 6; Length 629;

Best Local Similarity 91.2%; Pred. No. 1.8e-118;

Matches 530; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 1 ATGCCGACCCCAAGCTTCAACCCCAAGACACAGCGCTTATGAGCTTGTAGAGCTAT 60
Db 607 ATGCCGACCCCAAGCTTCCGCCCCAGACACAGCGCTTATGAGCTTGTAGAGCTAT 548
Qy 61 AGGCTGAGGAGAGAGGTTATGTCGTGAGCTGGGCTGAGGGAAGGCCCAAGCGCGAC 120
Db 547 AAGCTGAGGAGAGAGGTTATGTCGTGAGCTGGGCTGAGGGAAGGCCCAAGCGCTGAC 488
Qy 121 CCGCTGACCAAGCATCGGGCTGCTGAGACGAGTGTGAGACCCGTTTCCGCGCACCC 180
Db 487 CCGCTGACCAAGCATCGGGCTGCTGAGATGATGTTGAGACCCCGTTTCCGCGCACCC 428

Qy 181 TTCTGTACCTGGCGGCTCAGCTACAGTGAACCCAGGCTCAGCCCAAGAGCTTCACC 240
Db 427 TTCTGTATCTGGGGCTCAGCTGATGTGACCCAGGCTCAGCCCAACAAAGCTTCACC 368
Qy 241 CAGGTTTCCAGCAACTTTTCCAAAGGGGGCCCTTAACTGGGGCCGTCTTGTGGCACTTCTT 300
Db 367 CAGGTTTCCAGTAACTTTTCCAAAGGGGGCCCTTAACTGGGGCCGTCTTGTGGCACTTCTT 308
Qy 301 GTCTTTGGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGGGA 360
Db 307 GTCTTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAAGAAATGAGAACTGTGGGA 248
Qy 361 CAACTCCAGAGTTGGATCGTGGCCCTTACTGGAGACAGCTGTGGCTGATGTGATCCACAGC 420
Db 247 CAACTGCAAGAGTGGATGTGTGGCTTACTGGAGACAGCGGCTGTGCTGATGTGATCCACAGC 188
Qy 421 AGTGGCGGCTGGCGGCACTTCAACAGCTCTATACGGGGAACGGGGCCCTTGAAGAGCGACGG 480
Db 187 AGTGGGGGCTGGCGGAGTTTCAAGCTCTATACGGGGAACGGGGCCCTTGAAGAGCGCGG 128
Qy 481 CGTCTGCGGAGGGCACTGGGCACTGAGTGAACAAGTGTGACGGGGGCGGTGGCACTG 540
Db 127 CGTCTGCGGAGGGGAACCTGGGCACTGAGTGAACAAGTGTGACGGGGGCGGTGGCACTG 68
Qy 541 GGGGCCCTGTGTAAGTGTGAGGGCCCTTTTGTCTAGCAAGTG 581
Db 67 GGGGCATCTGTAACTGTAGGGGCCCTTTTGTCTAGCAAGTG 27

RESULT 9

AL157542 804 bp mRNA linear EST 04-SEP-2003

LOCUS AL157542

DEFINITION DKFZp761D0816 x1 761 (synonym: hamy2) Homo sapiens cDNA clone

DKFZp761D0816 5', mRNA sequence.

AL157542

AL157542.1 GI:7057943

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 804)

AUTHORS Ansoorge, W., Wilkner, U., Mewes, W., Weil, B. and Wiemann, S.

TITLE EST (Ansoorge, W., Wilkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;

Heidelberg, Germany) within the cDNA sequencing consortium of the

German Genome Project

No 81 sequence available.

This clone (DKFZp761D0816) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heuberweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

LOCATION/Qualifiers

1. 804

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp761D0816"

/issue_type="amygdala"

/dev_stage="adult"

/lab_host="DH10B"

/clone_id="761 (synonym: hamy2)"

/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 82.2%; Score 477.6; DB 1; Length 804;

Best Local Similarity 91.0%; Pred. No. 8.5e-113;
Matches 529; Conservative 0; Mismatches 50; Indels 2; Gaps 2;

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QY 1 ATGCCGACCCGACGCTCAACCCGACACACAGCGGCTCTGTAGTGTACTTTGTAGGCTAT 60
DB 134 ATGCCGACCCGACGCTCTGCGCCGACACACAGCGGCTCTGTAGTGTACTTTGTAGGCTAT 193
QY 61 AGGCTGAGGACAGAGGTTATGTCTGTGAGCTGCGGCTGCGGAGAGCCGACCGCGAC 120
DB 194 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGCGGCTGCGGAGAGGCGCCGACGACTGAC 253
QY 121 CCGCTGACACAGGCTATGCGGCTGCTGAGACGAGTTTGAAGCCGTTTCCGCGCAC 180
DB 254 CCGCTGACACAGGCTATGCGGCTGCTGAGAGTGTGAGACCGCTTCCGCGCAC 313
QY 181 TTCTGACCTGCGGCTGAGCTACGAGACGAGCCGACGCTGACGACGAGTTCAC 240
DB 314 TTCTGACCTGCGGCTGAGCTACGAGACGAGCCGACGCTGACGACGAGTTCAC 373
QY 241 CAGGTTTCGACGAACTTTTCCAGGCGGCTTAACTGCGGCTGCTTGTGCTATTTT 300
DB 374 CAGGTTTCGACGAACTTTTTCAGGCGGCTTAACTGCGGCTGCTTGTGCTATTTT 433
QY 301 GTCCTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 434 GTCCTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
QY 361 CAACTGCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 494 CAACTGCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
QY 421 AGTGGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 554 AGTGGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
QY 481 CGTCTGCGGAGGCGCACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 613 CGTCTGCGGAGGCGCACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
QY 541 GGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 581
DB 672 GGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
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RESULT 10
BP753530 1030 bp mRNA linear EST 20-SEP-2000
LOCUS 601590016P1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5',
DEFINITION mRNA sequence.
ACCESSION BE793530
VERSION BE793530.1 GI:10214832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1030)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LNCM800 row: p column: 04
High quality sequence start: 5
High quality sequence stop: 709.
Location/Qualifiers
1..1030

FEATURES
Source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3944307"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald W. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 82.1%; Score 477; DB 2; Length 1030;
Best Local Similarity 88.8%; Pred. No. 1.3e-112;
Matches 516; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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QY 1 ATGCCGACCCGACGCTCAACCCGACACACAGCGCTCTAGTGTACTTTGTAGGCTAT 60
DB 144 ATGCCGACCCGACGCTCTGCGCCGACACACAGCGGCTCTGTGCTGCTGCTGCTAT 203
QY 61 AGGCTGAGGACAGAGGTTATGTCTGTGAGCTGCGGCTGCGGAGAGCCGACCGCGAC 120
DB 204 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGCGGCTGCGGAGAGGCGCCGACGCTGAC 263
QY 121 CCGCTGACACAGGCTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 264 CCACTGACACAGGCTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 323
QY 181 TTCTGACCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 324 TTCTGACCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 383
QY 241 CAGGTTTCGACGAACTTTTCCAGGCGGCTTAACTGCGGCTGCTTGTGCTATTTT 300
DB 384 CAGGTTTCGACGAACTTTTTCAGGCGGCTTAACTGCGGCTGCTTGTGCTATTTT 443
QY 301 GTCCTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 444 GTCCTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503
QY 361 CAACTGCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 504 CAACTGCAAGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563
QY 421 AGTGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 564 AGTGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623
QY 481 CGTCTGCGGAGGCGCACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 624 CGTCTGCGGAGGCGCACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683
QY 541 GGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 581
DB 684 GGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 724
```

RESULT 11
BP753931 713 bp mRNA linear EST 08-JUL-2004
LOCUS BP753931
DEFINITION BP753931 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone m1a06063 5',
mRNA sequence.
ACCESSION BP753931
VERSION BP753931.1 GI:50073821
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 713)
AUTHORS Nishimura, M., Yokoi, N., Miki, T., Horikawa, Y., Yoshioka, H., Takeda, J., Ohara, O. and Seino, S.
TITLE Construction of a multi-functional cDNA library specific for mouse pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1. 713
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="m1a06063"
/sex="male"
/tissue_type="pancreatic islet"
/dev_stage="adult"
/clone_id="mouse (C57BL/6) pancreatic islet library with recombination-based method"

ORIGIN
Query Match 81.1%; Score 471.2; DB 5; Length 713;
Best Local Similarity 95.3%; Pred. No. 3.8e-111;
Matches 551; Conservative 0; Mismatches 18; Indels 9; Gaps 6;

2 TGCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGCTATA 61
Db TGGGAGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGCTATA 93
Qy 62 GCGTGAAGCAGAAAGGTTATGTCTGTGAGCTGGGCGCTGGGGAAGCCCGCCGAC 121
Db 94 AGCTGAGGACAGAAAGGTTATGTCTGTGAGCTGGGCGCTGGGGAAGCCCGCCGAC 153
Qy 122 GCGTGAAGCAGAAAGGTTATGTCTGTGAGCTGGGCGCTGGGGAAGCCCGCCGAC 181
Db 154 CGCTGACCAAGCATCGGCGCTCTGAGAGCGAGTTGAGACCCGTTCCGCGCACCT 213
Qy 182 TCTCTGACCTGGCGCTCAGCTACAGCGTGAACCCAGGCTCAGCCAGCAAGCTTCA 241
Db 214 TCTCTGACCTGGCGCTCAGCTACAGCGTGAACCCAGGCTCAGCCAGCAAGCTTCA 273
Qy 242 AGGTTTCCAGCAATTTTCCAGAGGGGCGCTTAACTGGGGCGCTTGTGGCAATCTTTG 301
Db 274 AGGTTTCCAGCAATTTTCCAGAGGGGCGCTTAACTGGGGCGCTTGTGGCAATCTTTG 333
Qy 302 TCTTTGGGGCGTGG -CCCTGTGTGCTGAGAGTGTCAAC -AAATAATGAGCCTTTGG -TG 357
Db 334 TCTTTGGGGCGTGGCGCTGTGTGTGAGAGTGTCAACAAATAATGAGCCTTTGGTGG 393
Qy 358 GGAACAATCCAGATTGG -ATCGTGGCTTACT -GGAGACACCTGTGGCTGACTGATC 414
Db 394 GGAACAATCCAGATTGGAGATTGGGCTTACTGCTGGAGACACCTGTGGCTGATGATC 453
Qy 415 CACAGCAGTGGCGG -CTGGGCGGACTTCAAGCTCTATACGGGGAAGGGGCGCTGAGG 472
Db 454 CACAGCAGTGGGCGGCTGGGCGGAGTTCAAGCTCTATACGGGGAAGGGGCGCTGAGG 513
Qy 473 ACGAGCGGCGCTTCCGGGAGGGGCAATGGGGCATAGAGAGCAAGTGTGACGGGGCGG 532
Db 514 ACGAGCGGCGCTTCCGGGAGGGGCAATGGGGCATAGAGAGCAAGTGTGACGGGGCGG 573
Qy 533 TGGCACTGGGGCGCTGTGTAAGTGAAGGCGCTTTT 570
Db 574 TGGCACTGGGGCGCTGTGTAAGGCGCTTTT 611

RESULT 12
LOCUS CK359685
DEFINITION AGENCOURT 17156314 NIH MGC 233 Rattus norvegicus cDNA clone
IMAGE:7105621 5', mRNA sequence.
CK359685
ACCESSION CK359685.1 GI:40325617
VERSION EST.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 757)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Daniela S. Gerhard, Ph.D.
COMMENT Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgs@nci.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM14965 row: a column: 11
High quality sequence start: 20
High quality sequence stop: 702.
Location/Qualifiers
1. 757
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7105621"
/tissue_type="heart, pooled"
/lab_host="DH10B Tona"
/clone_id="NIH MGC 233"
/note="Organ: heart; Vector: pExpress-1; Site: 1; EcoRV; Site 2: NotI; RNA obtained from pooled heart tissue from a mix of male and female animals at 8 wk old. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (TRI-reagent method). cDNA was primed using oligo-dT primer:
5'-pGACTAGTTTATATGTCGTGAGCTGGGCTGGGAAGGCCAGCCGAC 120
the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2 kb. This primary library is not normalized (normalized primary library is NIH MGC 234) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN
Query Match 78.6%; Score 456.6; DB 7; Length 757;
Best Local Similarity 95.9%; Pred. No. 2.3e-107;
Matches 490; Conservative 0; Mismatches 19; Indels 2; Gaps 2;

1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db 233 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 292
Qy 61 AGGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGGCTGGGAAGGCCAGCCGAC 120
Db 293 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGGCTGGGAAGGCCAGCCGAC 352
Qy 121 CCGCTGACCAAGCCATGCGGGCTGTGAGAGCAGATTGAGACCCGTTTCCGCGGAC 180
Db 353 CCGCTGACCAAGCCATGCGGGCTGTGAGAGCAGATTGAGACCCGTTTCCGCGGAC 412

QY 181 TTCTGACCTGCGCCCTGACGTACACGTGACCCAGGCTCAGCCAGACAGCTTCACC 240
Db 413 TTCTGACCTGCGCCCTGACGTACACGTGACCCAGGCTCAGCCAGACAGCTTCACC 472
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCTTACTGAGGCGCTTGTGACATTTCTT 300
Db 473 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCTTACTGAGGCGCTTGTGACATTTCTT 532
QY 301 GTCTTTGGGGGCTGCGCTGATGCTGAGATGTCACAAAGAAATGAGCTTTGTGTGGGA 360
Db 533 GTCTTTGGGGGCTGCGCTGATGCTGAGATGTCACAAAGAAATGAGCTTTGTGTGGGA 592
QY 361 CAAGTCACGAGTTGATCTGTCGCTTACCTGAGACACGTCGTGCTGACTGATCCACAGC 420
Db 593 CAAGTCACGAGTTGATCTGTCGCTTACCTGAGACACGTCGTGCTGACTGATCCACAGC 652
QY 421 AGTGGCGGCTGCGGCGGACCTTCAACGTCCTATACGGGAGCGGGGCGCTTGTGAGGACGACG 480
Db 653 AGTGGCGGCTGCGGCGGACCTTCAACGTCCTATACGGGAGCGGGGCGCTTGTGAGGACGACG 711
QY 481 CGTCTGCGGAGGCGCAACTGGGCGATGATGA 511
Db 712 CGTCTGCGGAGGCG-GACTGGGCACTGATGA 741

RESULT 13
CN281020 643 bp mRNA linear EST 16-MAY-2004
LOCUS 17000531876837 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN281020
ACCESSION CN281020.1 GI:47297434
VERSION EST.
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 643)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G., J.,
Li, Y., Xu, C., Fann, R., Guejler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 643 Std Error: 0.00.
Location/Qualifiers

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/cbase_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_id="GRN_EB"
/note="oligo dr primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p2), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN
Query Match 78.5%; Score 456; DB 7; Length 643;
Best Local Similarity 90.7%; Pred. No. 3.2e-107;
Matches 486; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACAGCGCTTACTAGTGGCTGACTTTGTAGGCTAT 60
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QY 61 AGCTGAGGCGAAGGGTTATGTTGTGTGAGCTGCGCTTGGGAGAGGCCAGCCGCGAC 120
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QY 121 CCGCTGACCAAGGCATGCGGGCTGTGAGAGAGAGTTTGAAGCCCGTTCCCGCGAC 180
Db 228 CCGCTGACCAAGGCATGCGGGCTGTGAGAGAGAGTTTGAAGCCCGTTCCCGCGAC 287
QY 181 TTCTGACCTGCGCCCTGACGTACACGTGACCCAGGCTCAGCCAGACAGCTTCACC 240
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QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCTTACTGAGGCGCTTGTGACATTTCTT 300
Db 348 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCTTACTGAGGCGCTTGTGACATTTCTT 407
QY 301 GTCTTTGGGGGCTGCGCTGATGCTGAGATGTCACAAAGAAATGAGCTTTGTGTGGGA 360
Db 408 GTCTTTGGGGGCTGCGCTGATGCTGAGATGTCACAAAGAAATGAGCTTTGTGTGGGA 467
QY 361 CAAGTCACGAGTTGATCTGTCGCTTACCTGAGACACGTCGTGCTGACTGATCCACAGC 420
Db 468 CAAGTCACGAGTTGATCTGTCGCTTACCTGAGACACGTCGTGCTGACTGATCCACAGC 527
QY 421 AGTGGCGGCTGCGGCGGACCTTCAACGTCCTATACGGGAGCGGGGCGCTTGTGAGGACGACG 480
Db 528 AGTGGCGGCTGCGGCGGACCTTCAACGTCCTATACGGGAGCGGGGCGCTTGTGAGGACGACG 587
QY 481 CGTCTGCGGAGGCGCAACTGGGCGATGATGATGACACAGTGTGACGCGGGCGCTGTGC 536
Db 588 CGTCTGCGGAGGCGCAACTGGGCGATGATGATGACACAGTGTGACGCGGGCGCTGTGC 643

RESULT 14
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LOCUS 56057475H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD617892
ACCESSION CD617892
VERSION CD617892.1 GI:40266157
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 662)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com
Location/Qualifiers

FEATURES
source
1..662
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_id="FLP"
/note="Vector: pDrive Cloning Vector"

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Query Match 77.1%; Score 447.8; DB 6; Length 662;
Best Local Similarity 90.2%; Pred. No. 4.3e-105;
Matches 490; Conservative 0; Mismatches 52; Indels 1; Gaps 1;

QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACAGCGCTTACTAGTGGCTGACTTTGTAGGCTAT 60
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QY 61 AGCTGAGGCGAAGGGTTATGTTGTGTGAGCTGCGCTTGGGAGAGGCCAGCCGCGAC 120

Db 180 AAGCTGAGGAGGATTAATGCTGTGAGAGCTGGAGCCCGGGGAGGGCCAGACAGCTGAC 239
Qy 121 CCGCTGACCAAGGATGATGCTGTGAGAGAGATTTGAGACCCGTTTCCGCGCAGC 180
Db 240 CCGCTGACCAAGGATGATGCTGTGAGAGATTTGAGACCCGTTTCCGCGCAGC 239
Qy 181 TTCTCTACCTGAGCCGCTGAGCTACAGTGAACCCAGGCTCAGCCAGCAAGCTTCAAC 240
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Qy 361 CAACTCCAGGATTTGATGCTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
Db 480 CAACTCCAGGATTTGATGCTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539
Qy 420 CAGTGGCGGCTGGGCGGAGCTTACAGCTCTATACGGGAGCGGGCCCTGAGAGAGAGAG 479
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Db 600 GCGTCTCGGGAGGGGCACTGGGCAATGAGTGAAGACAGTGTGACGGGGGCGCTGGGCACT 659
Qy 540 GGG 542
Db 660 GGG 662

RESULT 15

CD617890 627 bp mRNA linear EST 12-JAN-2004
LOCUS 56057367H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD617890
ACCESSION CD617890
VERSION CD617890.1 GI:40266155
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 627)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.

TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK

Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102

EMAIL: gfu@incyte.com
Location/Qualifiers

FEATURES
Source 1. 627
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 74.5%; Score 432.8; DB 6; Length 627;
Best Local Similarity 90.7%; Pred. No. 3.3e-101;
Matches 461; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
Qy 1 ATGCCGACCCCAAGCTTCAAGCCAGACAGACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db 120 ATGGCGACCCCAAGCTTCAAGCCAGACAGACAGCGGCTCTGGTGGCAGACTTTGTAGGCTAT 179

Qy 61 AAGCTGAGGAGGATTAATGCTGTGAGAGAGCTGGAGCCCGGGGAGGGCCAGACAGCTGAC 120
Db 180 AAGCTGAGGAGGATTAATGCTGTGAGAGAGCTGGAGCCCGGGGAGGGCCAGACAGCTGAC 239
Qy 121 CCGCTGACCAAGGATGATGCTGTGAGAGAGATTTGAGACCCGTTTCCGCGCAGC 180
Db 240 CCGCTGACCAAGGATGATGCTGTGAGAGAGATTTGAGACCCGTTTCCGCGCAGC 239
Qy 181 TTCTCTACCTGAGCCGCTGAGCTACAGTGAACCCAGGCTCAGCCAGCAAGCTTCAAC 240
Db 300 TTCTCTATCTGGGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCAAC 359
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Qy 301 GTCTTTGGGGCTGCTGCTGTGCTGAGAGTGTCAAAAGAAATGAGCCCTTGGTGGGA 360
Db 420 GTCTTTGGGGCTGCTGCTGTGCTGAGAGTGTCAAAAGAAATGAGCCCTTGGTGGGA 479
Qy 361 CAACTCCAGGATTTGATGCTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
Db 480 CAACTCCAGGATTTGATGCTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539
Qy 420 CAGTGGCGGCTGGGCGGAGCTTACAGCTCTATACGGGAGCGGGCCCTGAGAGAGAGAG 479
Db 540 CAGTGGCGGCTGGGCGGAGCTTACAGCTCTATACGGGAGCGGGCCCTGAGAGAGAGAG 599
Qy 480 GCGTCTCGGGAGGGGCACTGGGCAATGAGTGAAGACAGTGTGACGGGGGCGCTGGGCACT 539
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Search completed: April 10, 2005, 20:12:31
Job time: 2833.63 secs

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NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-897-3

Query Match 99.6%; Score 1005; DB 1; Length 193;
Best Local Similarity 99.5%; Pred. No. 8.5e-107;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MATPASTPTPRALVADPVGYKLRQKGYVCGAGGEGPADPLHQAARAAGDEFETFRRT 60
DB 1 MATPASTPTPRALVADPVGYKLRQKGYVCGAGGEGPADPLHQAARAAGDEFETFRRT 60
QY 61 FSDLAQLHVTTPGSAQORFTQVSDDELFOGSPMGRVAFVFGAALCAESVKNKEPPLVG 120
DB 61 FSDLAQLHVTTPGSAQORFTQVSDDELFOGSPMGRVAFVFGAALCAESVKNKEPPLVG 120
QY 121 QVQDMWVAVLETRLADWIHSSGMAEFTALYGDGALBEARRLRGNMASVRTLGAVAL 180
DB 121 QVQDMWVAVLETRLADWIHSSGMAEFTALYGDGALBEARRLRGNMASVRTLGAVAL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 3
US-08-978-523-3
Sequence 3, Application US/08978523
Patent No. 5863229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-523-3

Query Match 99.6%; Score 1005; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 8.5e-107;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MATPASTPTPRALVADPVGYKLRQKGYVCGAGGEGPADPLHQAARAAGDEFETFRRT 60
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QY 61 FSDLAQLHVTTPGSAQORFTQVSDDELFOGSPMGRVAFVFGAALCAESVKNKEPPLVG 120
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QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 4
US-08-978-897-5
Sequence 5, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Emmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483, 0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-798-897-5

Query Match 99.1%; Score 1000; DB 1; Length 192;
Best Local Similarity 99.5%; Pred. No. 3.2e-106;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 122 VQDMWVYLETRLADWTHSSGMAEFTALYGDGALBEARLRBGNMVASVTVLTGAVALG 181
DB 121 VQDMWVYLETRLADWTHSSGMAEFTALYGDGALBEARLRBGNMVASVTVLTGAVALG 180
QY 182 ALVTGAFPAK 193
DB 181 ALVTGAFPAK 192

RESULT 5
US-08-978-523-5
Sequence 5, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Emmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483, 0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-523-5

Query Match 99.1%; Score 1000; DB 2; Length 192;
Best Local Similarity 99.5%; Pred. No. 3.2e-106;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 121 VQDMWVYLETRLADWTHSSGMAEFTALYGDGALBEARLRBGNMVASVTVLTGAVALG 180
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DB 181 ALVTGAFPAK 192

RESULT 6
US-09-155-327G-7
Sequence 7, Application US/09155327G
Patent No. 6790637
GENERAL INFORMATION:
APPLICANT: AMRAD Operations Pty Ltd
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
FILE REFERENCE: 2096584
CURRENT APPLICATION NUMBER: US/09/155,327G
CURRENT FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: P8965
PRIOR FILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 7
LENGTH: 193
TYPE: PRT
ORGANISM: HUMAN
US-09-155-327G-7

Query Match 99.1%; Score 1000; DB 4; Length 193;
Best Local Similarity 99.0%; Pred. No. 3.2e-106;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MATPASTPDTRALVADPFVGYKLRQKGYCGAGPGEPPADPLHQMRAAGDEFETRFRRT 60
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DB 61 FSDLAQLHTVPGSAQGRFTQVSDELFGGPNMGRLVAFVFGAALCAESVKNKMEPLVQ 120
QY 121 QVDMWVYLETRLADWTHSSGMAEFTALYGDGALBEARLRBGNMVASVTVLTGAVAL 180
DB 121 QVDMWVYLETRLADWTHSSGMAEFTALYGDGALBEARLRBGNMVASVTVLTGAVAL 180
QY 181 GALVTGAFPAK 193
DB 181 GALVTGAFPAK 193

RESULT 7
US-09-949-016-10928

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; Sequence 10928, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10928
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10928

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Query Match          99.1%; Score 1000; DB 4; Length 193;
Best Local Similarity 99.0%; Pred. No. 3.2e-106;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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   |||
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QY 181 GALVTGAFPAASK 193
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Db 181 GALVTGAFPAASK 193
   |||

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RESULT 8
US-08-798-897-4
; Sequence 4, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-798-897-4

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Query Match          98.6%; Score 995; DB 1; Length 193;
Best Local Similarity 98.4%; Pred. No. 1.2e-105;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MATPASAPDRALVADPFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFEFRFRRT 60
   |||
QY 61 FSDLAQLHVTPTGSAQORFTQVSDELFOGPGPNWGRVAFVFGAALCAESVKNKMEPLVG 120
   |||
Db 61 FSDLAQLHVTPTGSAQORFTQVSDELFOGPGPNWGRVAFVFGAALCAESVKNKMEPLVG 120
   |||
QY 121 QVODMVAVLETRLDADMIHSSGMAEFTALYGDGALBEARRLRBNWASVRYTLTGAVAL 180
   |||
Db 121 QVODMVAVLETRLDADMIHSSGMAEFTALYGDGALBEARRLRBNWASVRYTLTGAVAL 180
   |||
QY 181 GALVTGAFPAASK 193
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Db 181 GALVTGAFPAASK 193
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RESULT 9
US-08-978-523-4
; Sequence 4, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid

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STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-523-4

Query Match 98.4%; Score 995; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 1,2e-105;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASADPTRALVADFTVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFETRFRRTF 60
DB 1 MATPASADPTRALVEDFTVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFETRFRRTF 60
QY 61 PSDLAQHLHTVPPGSAQOQFFTVSDLELFOGSPNMGRLVAFVFGAALCAESVKNKEBPLVG 120
DB 61 PSDLAQHLHTVPPGSAQOQFFTVSDLELFOGSPNMGRLVAFVFGAALCAESVKNKEBPLVG 120
QY 121 QVQDMVAVYLETBRLADWTHSSGMAEFPTALYGDGALBEARRLREGNMASVRTLGAVAL 180
DB 121 QVQDMVAVYLETBRLADWTHSSGMAEFPTALYGDGALBEARRLREGNMASVRTLGAVAL 180
QY 181 GALVTGAFPAK 193
DB 181 GALVTGAFPAK 193

RESULT 10
US-08-798-897-6
Sequence 6, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-798-897-6

Query Match 98.1%; Score 990; DB 1; Length 192;
Best Local Similarity 98.4%; Pred. No. 4.4e-105;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 ATPASTDTRALVADFTVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFETRFRRTF 61
DB 2 ATPASTDTRALVADFTVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFETRFRRTF 61

DB 1 ATPASADPTRALVEDFTVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFETRFRRTF 60
QY 62 SDLAQHLHTVPPGSAQOQFFTVSDLELFOGSPNMGRLVAFVFGAALCAESVKNKEBPLVG 121
DB 61 SDLAQHLHTVPPGSAQOQFFTVSDLELFOGSPNMGRLVAFVFGAALCAESVKNKEBPLVG 120
QY 122 VQDMVAVYLETBRLADWTHSSGMAEFPTALYGDGALBEARRLREGNMASVRTLGAVALG 181
DB 121 VQDMVAVYLETBRLADWTHSSGMAEFPTALYGDGALBEARRLREGNMASVRTLGAVALG 180
QY 182 ALVTGAFPAK 193
DB 181 ALVTGAFPAK 192

RESULT 11
US-08-978-523-6
Sequence 6, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-523-6

Query Match 98.1%; Score 990; DB 2; Length 192;
Best Local Similarity 98.4%; Pred. No. 4.4e-105;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 ATPASTDTRALVADFTVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFETRFRRTF 61
DB 1 ATPASADPTRALVEDFTVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFETRFRRTF 60
QY 62 SDLAQHLHTVPPGSAQOQFFTVSDLELFOGSPNMGRLVAFVFGAALCAESVKNKEBPLVG 121
DB 61 SDLAQHLHTVPPGSAQOQFFTVSDLELFOGSPNMGRLVAFVFGAALCAESVKNKEBPLVG 120
QY 122 VQDMVAVYLETBRLADWTHSSGMAEFPTALYGDGALBEARRLREGNMASVRTLGAVALG 181
DB 122 VQDMVAVYLETBRLADWTHSSGMAEFPTALYGDGALBEARRLREGNMASVRTLGAVALG 181

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Db      121 VQEMMVAVYETRLADWIHSSGNAEFTALYGGALAEARLREGWMAVRVLGAVALG 180
Qy      182 ALTVGAFFASK 193
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        181 ALTVGAFFASK 192

RESULT 12
US-09-155-327G-10
? Sequence 10, Application US/09155327G
? Patent No. 6790637
? GENERAL INFORMATION:
? APPLICANT: AMRAD Operations Pty Ltd
? TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
? FILE REFERENCE: 2096584
? CURRENT APPLICATION NUMBER: US/09/155,327G
? CURRENT FILING DATE: 1999-03-29
? PRIOR APPLICATION NUMBER: PN8965
? PRIOR FILING DATE: 1996-03-27
? NUMBER OF SEQ ID NOS: 15
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 10
? LENGTH: 333
? TYPE: PRT
? ORGANISM: murine
US-09-155-327G-10

Query Match      76.9%; Score 776; DB 4; Length 333;
Best Local Similarity 75.4%; Pred. No. 3e-80;
Matches 159; Conservative 5; Mismatches 17; Indels 30; Gaps 4;

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Db      1 MATPASTDPTALVADFVGYTLRKQGYVCGAGPGEGBPAADPLHQARRAGDEPETFRRFT 60
Qy      61 FSDLAAGQHTVPGSAOORFOVSDDELROGGPBMGRVAVFVFGALCAESVKEKEPLVG 120
Db      61 FSDLAAGQHTVPGSAOORFOVSDDELROGGPBMGRVAVFVFGALCAESVKEKEPLVG 120
Qy      121 QVQDMVAVYETRLADWIHSSGNAEFTALYG--DGLAEARLRLE----- 164
Db      121 QVQDMVAVYETRLADWIHSSGNAEFTALYG--DGLAEARLRLE----- 164
Qy      165 -GN-----MASVTVTLGAVALGA 182
Db      180 PGNAGPVIMSLERMEADARSIVYGNDYGA 210

RESULT 13
US-09-149-476-696
? Sequence 696, Application US/09149476
? Patent No. 6420526
? GENERAL INFORMATION:
? APPLICANT: Rosen et al.
? TITLE OF INVENTION: 186 Human Secreted proteins
? FILE REFERENCE: P2002P1
? CURRENT APPLICATION NUMBER: US/09/149,476
? CURRENT FILING DATE: 1998-09-08
? EARLIER APPLICATION NUMBER: PCT/US98/04493
? EARLIER FILING DATE: 1998-03-06
? EARLIER APPLICATION NUMBER: 60/040,162
? EARLIER FILING DATE: 1997-03-07
? EARLIER APPLICATION NUMBER: 60/040,333
? EARLIER FILING DATE: 1997-03-07
? EARLIER APPLICATION NUMBER: 60/038,621
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EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
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EARLIER APPLICATION NUMBER: 60/047,597
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06

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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,614
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EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
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EARLIER APPLICATION NUMBER: 60/047,501

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
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EARLIER APPLICATION NUMBER: 60/056,862
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EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 75.2%; Score 759; DB 4; Length 365;
Best Local Similarity 98.6%; Pred. No. 3e-78;
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MATPASTPDRALVADFGYKLRKGVCGAPGEGPAADPLHOMRAAGDEFTRRPRT 60
Db 1 MATPASAPDRALVADFGYKLRKGVCGAPGEGPAADPLHOMRAAGDEFTRRPRT 60
Qy 61 FSDLAOLHTYTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNEMEPVVG 120
Db 61 FSDLAOLHTYTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNEMEPVVG 120
Qy 121 QVDPNVAVYLETRLADWTHSSGCV 144
Db 121 QVDPNVAVYLETRLADWTHSSGCV 144

RESULT 14
US-09-010-147B-24
Sequence 24, Application US/09010147B
Patent No. 6553445
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: Human Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,147B
FILING DATE: 12-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-Jan-1997
APPLICATION NUMBER: US 60/034,204
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: PF353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-010-147B-24

Query Match 75.2%; Score 759; DB 4; Length 365;
Best Local Similarity 98.6%; Pred. No. 3e-78;
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFVGYKLRQKGYVCGAGPGGPAADPLHQMRAAGDEFETRRRT 60
DB 1 MATPASAPPTRALVADPFVGYKLRQKGYVCGAGPGGPAADPLHQMRAAGDEFETRRRT 60
QY 61 FSDLAQLHVTPEGSACQRFQVSDLEFQGGPVMGRVAFVFGAALCAESVKNKEMEPLVG 120
DB 61 FSDLAQLHVTPEGSACQRFQVSDLEFQGGPVMGRVAFVFGAALCAESVKNKEMEPLVG 120
QY 121 QVQDMVMVAYLETRLADWIHSSGGW 144
DB 121 QVQDMVMVAYLETRLADWIHSSGGW 144

RESULT 15
US-09-639-245-2
Sequence 2, Application US/09639245
Patent No. 6737511
GENERAL INFORMATION:
APPLICANT: Youle et al.
TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL
FILE REFERENCE: 4239-55417
CURRENT APPLICATION NUMBER: US/09/639,245
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/149,220
PRIOR FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: genetic fusion
US-09-639-245-2

Query Match 42.9%; Score 432.5; DB 4; Length 411;
Best Local Similarity 39.9%; Pred. No. 8.2e-41;
Matches 93; Conservative 26; Mismatches 63; Indels 51; Gaps 4;

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DB 26 RELVADPFVGYKLRQKGYVCGAGP-----GEGPAA 39
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DB 86 NGATRAHSSSLDARAVIPMAAVKQALREAGDEFETRRRAFSDLTSQHLITPGTAYQSFEQ 145
QY 82 VSDLEFQGGPVMGRVAFVFGAALCAESVKNKEMEPLVGQVQDMVMVAYLETRLADWIHSS 141
DB 146 VVNELEFRDGVVMGRVAFVFGAALCAESVKNKEMEPLVSRHIAAMATYLDHLEPWIQEN 205
QY 142 GGAAPFTALYDQALBEARLRRE--GNWASVRYTLTGAVALGALVTYVGAFFPAS 192
DB 206 GGMDFVELYGNNAABSRKQGERFRMFLTGMTVAGVVLGSLFSRKAYSAA 258

Search completed: April 10, 2005, 22:45:27
Job time : 19.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2005, 20:17:32 ; Search time 59 Seconds
(without alignments)
1675.106 Million cell updates/sec

Title: US-09-925-674B-9

Perfect score: 1009

Sequence: 1 MATPASTPDRALVADFPVGY.....LTGAVLGLVTGAFPSK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 1009 | 100.0 | 193 | 1 BCLW_MOUSE | P70345 mus musculi |
| 2 | 1005 | 99.6 | 193 | 2 Q88956 | Q88956 rattus norv |
| 3 | 1005 | 99.6 | 219 | 2 Q7S60 | Q7S60 rattus norv |
| 4 | 1000 | 99.1 | 193 | 1 BCLW_HUMAN | Q92844 homo sapien |
| 5 | 996 | 98.7 | 192 | 2 Q6A093 | Q6A093 mus musculi |
| 6 | 960 | 95.1 | 193 | 2 Q8CGL4 | Q8CGL4 mus musculi |
| 7 | 770 | 76.3 | 178 | 2 Q8CPR2 | Q8CPR2 mus musculi |
| 8 | 770 | 76.3 | 178 | 2 Q9CWS | Q9CWS mus musculi |
| 9 | 655.5 | 65.0 | 188 | 2 Q6GPR2 | Q6GPR2 xenopus lae |
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| 11 | 439.5 | 42.9 | 233 | 2 Q9MYW4 | Q9MYW4 oryctolagus |
| 12 | 432.5 | 42.9 | 229 | 1 BCLX_CHICK | Q07818 gallus galli |
| 13 | 432.5 | 42.9 | 233 | 2 Q8S042 | Q8S042 felis silve |
| 14 | 431.5 | 42.8 | 233 | 1 BCLX_PIG | Q77737 sus scrofa |
| 15 | 431.5 | 42.8 | 233 | 2 Q9N1A2 | Q9N1A2 sus scrofa |
| 16 | 428.5 | 42.5 | 233 | 1 BCLX_MOUSE | Q64373 mus musculi |
| 17 | 428.5 | 42.5 | 233 | 1 BCLX_MOUSE | P53563 rattus norv |
| 18 | 428.5 | 42.5 | 233 | 2 Q9M257 | Q9M257 ovis aries |
| 19 | 427.5 | 42.4 | 233 | 1 BCLX_HUMAN | Q07817 homo sapien |
| 20 | 427.5 | 42.4 | 233 | 2 Q761T7 | Q761T7 canis famli |
| 21 | 423.5 | 42.0 | 233 | 1 BCL2_CHICK | Q00709 gallus galli |
| 22 | 415.5 | 41.2 | 229 | 1 BCL2_BOVIN | Q02718 bos taurus |
| 23 | 413 | 40.8 | 236 | 1 BCL2_RAT | P49950 rattus norv |
| 24 | 412 | 40.8 | 236 | 1 BCL2_MOUSE | P10417 mus musculi |
| 25 | 412 | 40.8 | 236 | 2 Q7TSK8 | Q7TSK8 rattus norv |
| 26 | 412 | 40.8 | 236 | 2 Q9B0R4 | Q9B0R4 mus musculi |
| 27 | 411.5 | 40.8 | 239 | 1 BCL2_HUMAN | P10413 homo sapien |
| 28 | 406 | 40.2 | 79 | 2 Q7S61 | Q7S61 rattus norv |
| 29 | 402 | 39.8 | 236 | 1 BCL2_CRITO | Q9156 cricetus |
| 30 | 401.5 | 39.8 | 239 | 2 Q7S5V7 | Q7S5V7 canis famli |
| 31 | 401 | 39.7 | 180 | 2 Q9BDD5 | Q9BDD5 bos taurus |

| | | | | | |
|----|-------|------|-----|--------------|--------------------|
| 32 | 401 | 39.7 | 217 | 2 Q9N35 | Q9N35 mus musculi |
| 33 | 400 | 39.6 | 238 | 2 Q90298 | Q90298 brachydanio |
| 34 | 398.5 | 39.5 | 180 | 2 Q9BDX7 | Q9BDX7 bos taurus |
| 35 | 398 | 39.4 | 236 | 2 Q923K6 | Q923K6 cricetus |
| 36 | 396.5 | 39.3 | 201 | 2 Q6G1L5 | Q6G1L5 xenopus tro |
| 37 | 395.5 | 39.2 | 235 | 2 Q81008 | Q81008 felis silve |
| 38 | 395 | 39.1 | 236 | 2 Q6R755 | Q6R755 canis famli |
| 39 | 380.5 | 37.7 | 284 | 2 Q7S62 | Q7S62 rattus norv |
| 40 | 374.5 | 37.1 | 188 | 2 Q9QW2 | Q9QW2 mus musculi |
| 41 | 374.5 | 37.1 | 235 | 2 Q35843 | Q35843 mus musculi |
| 42 | 372.5 | 36.9 | 188 | 2 Q9H1R6 | Q9H1R6 homo sapien |
| 43 | 371 | 36.8 | 204 | 2 Q902H2 | Q902H2 xenopus lae |
| 44 | 369 | 36.6 | 204 | 1 ARI1_XENLA | Q91828 xenopus lae |
| 45 | 365.5 | 36.2 | 153 | 2 Q7YB6 | Q7YB6 canis famli |

ALIGNMENTS

| RESULT 1 | BCLW_MOUSE | STANDARD | PRT | 193 AA. |
|----------|--|----------|-----|---------|
| AC | P70345; | | | |
| AD | 01-NOV-1997 (Rel. 35, Created) | | | |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) | | | |
| DT | 05-JUL-2004 (Rel. 44, Last annotation update) | | | |
| DE | Apoptosis regulator Bcl-w (Bcl-2-like 2 protein). | | | |
| GN | Name=Bcl2l2; Synonym=Bclw; | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEBLIN=96358615; PubMed=6761287; | | | |
| RA | Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G., | | | |
| RA | Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S., | | | |
| RT | "bcl-w", a novel member of the bcl-2 family, promotes cell survival.," | | | |
| RL | Oncogene 13:665-675 (1996). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=CS7BL/10J; | | | |
| RX | MEBLIN=98160183; PubMed=9500547; | | | |
| RA | Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K., | | | |
| RA | Russell L.D., Macgregor G.R.," | | | |
| RT | "Testicular degeneration in Bclw-deficient mice.," | | | |
| RL | Nat. Genet. 18:251-256 (1998). | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=CS7BL/6J; TISSUE=Testis; | | | |
| RX | MEBLIN=22354683; PubMed=1246851; DOI=10.1038/nature01266; | | | |
| RA | Okazaki Y., Furuno M., Kaenaka T., Adachi J., Bono H., Kondo S., | | | |
| RA | Nikaido I., Osato N., Saito R., Suzuki H., Yamanka I., Kiyosawa H., | | | |
| RA | Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T., | | | |
| RA | Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.W., | | | |
| RA | Schirni L.M., Kanapin A., Matsuda H., Batatov S., Betzel K.W., | | | |
| RA | Blake J.M., Bradt D., Brusic V., Chochia C., Coridan L.B., Cousins S., | | | |
| RA | Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., | | | |
| RA | Gaesteland T., Gariboldi M., Gissi C., Godzik A., Gough J., | | | |
| RA | Grimmond S., Guetlich S., Hirokawa N., Jackson I.J., Jarvis E.D., | | | |
| RA | Kanai A., Kawai H., Kawasawa Y., Kedziercki R.M., King B.L., | | | |
| RA | Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., | | | |
| RA | Mogilic D.R., Maltais L., Marchionni L., McKenzie L., Miki H., | | | |
| RA | Nagashima T., Numata K., Okido T., Pavan W.J., Petosa G., Pesole G., | | | |
| RA | Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., | | | |
| RA | Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., | | | |
| RA | Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K., | | | |
| RA | Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., | | | |
| RA | Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C., | | | |
| RA | Wilmig L.G., Wynshaw-Boris A., Yamagisawa M., Yang I., Yang L., | | | |
| RA | Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., | | | |
| RA | Hirozane-Kihikawa T., Kono H., Nakamura M., Sakazume N., Sato K., | | | |
| RA | Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., | | | |

RA Hara A., Hashizume W., Imotani K., Iehi Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs." Nature 420:563-573 (2002).
RL Nature 420:563-573 (2002).
CC -1- FUNCTION: Promotes cell survival.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC in a wide range of tissues, with highest levels in brain, colon,
CC and salivary gland.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -----
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CC -----
DR EMBL: U59746; AAB09056.1; -
DR EMBL: AF030769; AAB86430.1; -
DR EMBL: AK015644; BAB29912.1; -
DR HSSP: Q92843; 100L.
DR MGD: MGI:108052; Bcl2.12.
DR GO: GO:0005515; P:protein binding, IPT.
DR GO: GO:0006915; P:apoptosis, IDA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01260; BH4; 1; 1.
DR PROSITE: PSS0063; BH4_2; 1.
DR KX Apoptosis.
FT DOMAIN 9 29 BH4.
FT DOMAIN 85 104 BH1.
FT DOMAIN 136 151 BH2.
SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;

Query Match 100.0%; Score 1009; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.5e-82;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASTDPTALVADPVGYKLRKGYVCGAPGEGPAADPLHQAMBAAGDEPTFRRT 60
DB 1 MATPASTDPTALVADPVGYKLRKGYVCGAPGEGPAADPLHQAMBAAGDEPTFRRT 60
QY 61 FSDLAALQHTVPGSAQQRFTVDSDELROGGNNKRLVAFVFGAALCAESVNTKMEPLV 120
DB 61 FSDLAALQHTVPGSAQQRFTVDSDELROGGNNKRLVAFVFGAALCAESVNTKMEPLV 120
QY 121 QVDDMVVAAYLETRLADWTHSSGVAEFALYGDGALREARLRBGNNASTRVLTGAVNL 180
DB 121 QVDDMVVAAYLETRLADWTHSSGVAEFALYGDGALREARLRBGNNASTRVLTGAVNL 180
QY 181 GALTVAAGFFASK 193
DB 181 GALTVAAGFFASK 193

ID 088996 PRELIMINARY; PRT; 193 AA.
AC 088996;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Bcl-w (Hypothetical protein).
GN Name=bcl-w;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=99292146; PubMed=10366024; DOI=10.1016/S0306-4522(98)00642-3;
RA Hammer S., Skoglosa Y., Lindholm D.;
RT "Differential expression of bcl-w and bcl-x messenger RNA in the
RT developing and adult rat nervous system.";
RL Neuroscience 91:673-684 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22672518; PubMed=12787069;
RA Itoh T., Itoh A., Pleasure D.;
RT "Bcl-2-related protein family gene expression during oligodendroglial
RT differentiation.";
RL J. Neurochem. 85:1500-1512 (2003).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
RA Villard D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF096291; AAC64200.1; -
DR EMBL: AY185098; AAC64468.1; -
DR EMBL: BC074021; AAH74021.1; -
DR HSSP: Q92943; 100L.
DR GO: GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01260; BH4; 1; 1.
DR PROSITE: PSS0063; BH4_2; 1.

KW Hypothetical protein.
SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AF84 CRC64;

Query Match 99.6%; Score 1005; DB 2; Length 193;

Best Local Similarity 99.5%; Pred. No. 5.8e-82;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADPFVGYTLRQKGYCGAGPGEPAADPLHOAMRAAGDEFETRRPRT 60
DB 1 MATPASTPDTRALVADPFVGYTLRQKGYCGAGPGEPAADPLHOAMRAAGDEFETRRPRT 60
QY 61 FSDIAAQLHVTTPGSAQORFTQVSDLELFGQGNMGRVAFVFGAALCAESVYKMEPLVG 120
DB 61 FSDIAAQLHVTTPGSAQORFTQVSDLELFGQGNMGRVAFVFGAALCAESVYKMEPLVG 120
QY 121 QVQDMNTYLETRLADWIHSSGWAFFETALYGDALBEARLRBGNMNAVTTVLTGAVAL 180
DB 121 QVQDMNTYLETRLADWIHSSGWAFFETALYGDALBEARLRBGNMNAVTTVLTGAVAL 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193

RESULT 3

ID Q7TS60 PRELIMINARY; PRT; 219 AA.
AC Q7TS60;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE BCL-WBL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22672518; PubMed=12787069;
RA Itoh T., Itoh A., Pleasure D.;
RT "Bcl-2-related protein family gene expression during oligodendroglial
RT differentiation.";
RL J. Neurochem. 85:1500-1512(2003).
DR EMBL; AY185100; AA064470.1; -.
DR HSP; Q07817; IR2D.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00453; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 219 AA; 23720 MW; 30E36041BC1DC66F CRC64;

Query Match 99.6%; Score 1005; DB 2; Length 219;

Best Local Similarity 99.5%; Pred. No. 6.7e-82;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADPFVGYTLRQKGYCGAGPGEPAADPLHOAMRAAGDEFETRRPRT 60
DB 27 MATPASTPDTRALVADPFVGYTLRQKGYCGAGPGEPAADPLHOAMRAAGDEFETRRPRT 86
QY 61 FSDIAAQLHVTTPGSAQORFTQVSDLELFGQGNMGRVAFVFGAALCAESVYKMEPLVG 120
DB 87 FSDIAAQLHVTTPGSAQORFTQVSDLELFGQGNMGRVAFVFGAALCAESVYKMEPLVG 146

QY 121 QVQDMNTYLETRLADWIHSSGWAFFETALYGDALBEARLRBGNMNAVTTVLTGAVAL 180
DB 147 QVQDMNTYLETRLADWIHSSGWAFFETALYGDALBEARLRBGNMNAVTTVLTGAVAL 206
QY 181 GALVTGAFPAASK 193
DB 207 GALVTGAFPAASK 219

RESULT 4

ID BCLW_HUMAN STANDARD; PRT; 193 AA.
AC Q92843;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Apoptosis regulator Bcl-w (Bcl-2-like 2 protein).
GN Name=BCL2L2; Synonyms=BCLW, KIAA0271;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT "Bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL Oncogene 13:665-675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";
RL DNA Res. 3:321-329(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hulton B., Ketterman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywnicki M.I., Skalska U., Smillie D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Promotes cell survival.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC in a wide range of tissues, with highest levels in brain, colon,
CC and salivary gland.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -----
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 CC -----
 DR EMBL: U9747; AAB09055.1; -
 DR EMBL: D87461; BAA19666.2; ALT_INIT.
 DR EMBL: BC021198; AAH21198.1; -
 DR PDB: 1MK3; NMR; A=2-172.
 DR PDB: 100L; NMR; A=1-183.
 DR Genew; HGNC:995; BCL2L2.
 DR H-InvDB; HIX0011536; -
 DR MIM; 601931; -
 DR GO; GO:0005737; Cytoplasm; NAS.
 DR GO; GO:0006916; P:anti-apoptosis; TAS.
 DR GO; GO:0007283; P:spermatogenesis; TAS.
 DR InterPro; IPR000712; Bcl2 BH.
 DR InterPro; IPR003093; Bcl2 BH4.
 DR InterPro; IPR002475; BCL2_family.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS0063; BH4_2; 1.
 DR 3D-structure; Apoptosis.
 FT DOMAIN 9 29 BH4.
 FT FT 85 104 BH1.
 FT FT 136 151 BH2.
 SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;
 Query Match 99.1%; Score 1000; DB 1; Length 193;
 Best Local Similarity 99.0%; Pred. No. 1,6e-81;
 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MATPASTPTDTRALVADFGVGYKLRQKGYVCGAGPGEPPADPLHQMRAAGDEFFTRRPT 60
 DB 1 MATPASTPTDTRALVADFGVGYKLRQKGYVCGAGPGEPPADPLHQMRAAGDEFFTRRPT 60
 QY 61 FSDLAALQHTVTPGSAQORFTQVSDLFQGGPWGRLVAFVFGAALCAESVKNKMEPLVG 120
 DB 61 FSDLAALQHTVTPGSAQORFTQVSDLFQGGPWGRLVAFVFGAALCAESVKNKMEPLVG 120
 QY 121 QVQDMWVAYLETRLDWTHSSGMAEFTALYGDGALBEARLRGNMNAVTVLTGVAL 180
 DB 121 QVQDMWVAYLETRLDWTHSSGMAEFTALYGDGALBEARLRGNMNAVTVLTGVAL 180
 QY 181 GALVTVGAFPAK 193
 DB 181 GALVTVGAFPAK 193
 Db 181 GALVTVGAFPAK 193
 RESULT 5
 ID 06A093 PRELIMINARY; PRT; 192 AA.
 AC 06A093;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DE MK1AA0271 protein (Fragment).
 GN Name=MK1AA0271;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Okazaki N., Kikuno R.F., Ohara R., Iamato S., Koseki H., Hiraoka S.,
 RA Suga Y., Sano S., Nishimura M., Kato T., Hoshino K., Kitamura H.,
 RA Nagase T., Ohara O., Koga H.,
 RT Prediction of the Coding Sequences of Mouse Homologues of KIA Gene:
 RT IV. The Complete Nucleotide Sequences of 500 Mouse KIA-Homologous
 RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
 RT Randomly Sampled from Size-Fractionated Libraries.";
 RL DNA Res. 11:205-218(2004).
 DR EMBL: AK172925; BDD32203.1; -
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0006915; P:apoptosis; IDA.
 DR InterPro; IPR000712; Bcl2 BH.
 DR InterPro; IPR003093; Bcl2 BH4.
 DR InterPro; IPR002475; BCL2_FAMILY.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS0063; BH4_2; 1.
 DR NON_TER 1
 FT 1
 SQ SEQUENCE 192 AA; 20763 MW; A56CE4BC51D41F8A CRC64;
 Query Match 98.7%; Score 996; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 3.7e-81;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATPASTPTDTRALVADFGVGYKLRQKGYVCGAGPGEPPADPLHQMRAAGDEFFTRRPT 60
 DB 2 MATPASTPTDTRALVADFGVGYKLRQKGYVCGAGPGEPPADPLHQMRAAGDEFFTRRPT 61
 QY 61 FSDLAALQHTVTPGSAQORFTQVSDLFQGGPWGRLVAFVFGAALCAESVKNKMEPLVG 120
 DB 62 FSDLAALQHTVTPGSAQORFTQVSDLFQGGPWGRLVAFVFGAALCAESVKNKMEPLVG 121
 QY 121 QVQDMWVAYLETRLDWTHSSGMAEFTALYGDGALBEARLRGNMNAVTVLTGVAL 180
 DB 122 QVQDMWVAYLETRLDWTHSSGMAEFTALYGDGALBEARLRGNMNAVTVLTGVAL 181
 QY 181 GALVTVGAF 190
 DB 182 GALVTVGAF 191
 Db 182 GALVTVGAF 191
 RESULT 6
 ID 08CG14 PRELIMINARY; PRT; 193 AA.
 AC 08CG14;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DE Bcl2-like protein 2.
 GN Name=Bcl212;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6; TISSUE=Skin;
 RA Su H.-Y., Cheng W.T.K., Chen S.C., Lin C.T., Lien Y.Y., Liu H.J.,
 RA Gilmour R.S.;
 RT "Mouse keratinocytes express c98, a novel gene homologous to bcl-2,
 RT that is stimulated by insulin-like growth factor 1 and prevents
 RT dexamethasone-induced apoptosis.";
 RL Biochim. Biophys. Acta 1676:127-137(2004).
 DR EMBL: AY170344; AA013177.2; -
 DR HSSP; 092843; 100L.
 DR MGD; MGI:108052; Bcl212.

RA the FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Suganaka Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630 (2000).

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Suni N., Akiyama J., Nishi K., Kiteunat T., Tashiro H., Itoh M.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771 (2000).

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Akehawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki K., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasakawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kuribara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,
RA Sano H., Sasaki D., Shihata K., Saito K., Saito R., Sakai C., Sakai K.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi A., Shiraki T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AK013244; BAB28740.1; -
DR HSSP: Q92843; 100L.
DR WGD; MGI:108052; Bcl212.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:000515; F:protein binding; IPT.
DR GO; GO:0006915; P:apoptosis; IDA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01260; BH4_2; 1.
DR PROSITE; PSS0063; BH4_2; 1.
SQ SEQUENCE 178 AA; 15147 MW; E2D4G3F79528E9D7 CRC64;

Query Match Best Local Similarity 76.3%; Score 770; DB 2; Length 178;
Matches 145; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MATPASTPDRATVADVEVGYKLRQKGVYCGAGPGEPPADPLQAMRAAGDEFFTRFRRT 60
DB 1 MATPASTPDRATVADVEVGYKLRQKGVYCGAGPGEPPADPLQAMRAAGDEFFTRFRRT 60
QY 61 FSDIAAQLHTVTPGSAOQRFVQSDDELFOGGPNMGRVAFVFFGALCAESVKNKEPVLV 120
DB 61 FSDIAAQLHTVTPGSAOQRFVQSDDELFOGGPNMGRVAFVFFGALCAESVKNKEPVLV 120

QY 121 QVQDMWVATLETRLDWTHSSGWAEPYAL 150
DB 121 QVQDMWVATLETRLDWTHSSGWAEPYAL 150

RESULT 9
ID 06GP82 PRELIMINARY; PRT; 188 AA.
AC 06GP82;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGCB0617 protein.
OS Name=MGCB0617;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OK NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bock S.S., Loggellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
RA Richardson D.K., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hailton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Skalska U., Smallus D.E., Schermer A., Schein J.E.,
RA Krzywnicki M.I., Skalska U., Smallus D.E., Schermer A., Schein J.E.,
RA Jones S.J., Maier M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391 (2002).

RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073259; AAH73259.1; -
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
SQ SEQUENCE 188 AA; 20441 MW; CB3C1A8C55F16B96 CRC64;

Query Match 65.0%; Score 655.5; DB 2; Length 188;

Best Local Similarity 69.4%; Pred. No. 1.1e-50;
Matches 127; Conservative 19; Mismatches 34; Indels 3; Gaps 1;

QY 11 RALVADPVGYKLRQKGYVCGAGPBGPAADPLHQARAAAGDEPFRFRRTSDLAQQLH 70
Db 9 RALVEDVRYKLCQRLV---PEPAGPASCALHSAMRAAGDEFEFRFRQAQSEISTQIH 65
QY 71 TPQSAQORFTQVSDLEFQGGPVMGRVAFVFGAALCAESVKNKEMEPVGVQVDMVAVYL 130
Db 66 TPQTAVARFAEVAAGSLFQGGVNMGRVAFVFGAALCAESVKNKEMEPVGVQVDMVAVYL 125
QY 131 ETRLDADWISSGMAEFTALYGDGALBEARLRREGNMAVRYTLTGAVNLGALTVCAGF 190
Db 126 ETRLDADWISSGMAEFTALYGDGALBEARLRREGNMAVRYTLTGAVNLGALTVCAGF 185
QY 191 ASK 193
Db 186 ASK 188

RESULT 10
ARI_XENLA STANDARD; PRT; 228 AA.

AC 091827;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 23-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator R1 (XRI) (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
NC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Head;
RX MEDLINE=95331613; PubMed=7607538; DOI=10.1016/0378-1119(95)00159-4;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RT cell-survival genes.";
RL Gene 158:171-179(1995).
CC -1- FUNCTION: Could be the homolog of mammalian Bcl-W.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (potential).
CC -1- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the
CC brain of mid-metamorphic to post-metamorphic tadpoles and
CC adults, where an increase of several fold has been observed.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X83462; CA57845.1; -
CC HSSP: Q07817; 1MAZ.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR Apoptosis; Transmembrane.
KW NON_TER 1
FT DOMAIN 120 139 BH1.
FT DOMAIN 171 186 BH2.
FT TRANSMEM 207 227 Potential.

SEQ SEQUENCE 228 AA; 25068 MW; C49D449A585F8A9 CRC64;

Query Match 64.5%; Score 650.5; DB 1; Length 228;
Best Local Similarity 68.5%; Pred. No. 3.9e-50;
Matches 126; Conservative 20; Mismatches 35; Indels 3; Gaps 1;

QY 10 TRALVADPVGYKLRQKGYVCGAGPBGPAADPLHQARAAAGDEPFRFRRTSDLAQQLH 69
Db 48 SRALVEDVRYKLCQRLV---PEPAGPASCALHSAMRAAGDEFEFRFRQAQSEISTQIH 104
QY 70 TPQSAQORFTQVSDLEFQGGPVMGRVAFVFGAALCAESVKNKEMEPVGVQVDMVAVYL 129
Db 105 TPQTAVARFAEVAAGSLFQGGVNMGRVAFVFGAALCAESVKNKEMEPVGVQVDMVAVYL 164
QY 130 ETRLDADWISSGMAEFTALYGDGALBEARLRREGNMAVRYTLTGAVNLGALTVCAGF 189
Db 165 ETRLDADWISSGMAEFTALYGDGALBEARLRREGNMAVRYTLTGAVNLGALTVCAGF 224
QY 190 FASK 193
Db 225 FASK 228

RESULT 11

ID 09MYM4 PRELIMINARY; PRT; 233 AA.

AC 09MYM4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Bcl-X.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Knott J.C., Robertson L., James E.R.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY005131; AAF88137.1; -
DR HSSP: P53563; 1AF3.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01258; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS50063; BH4; 2; 1.
SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

Query Match 43.6%; Score 439.5; DB 2; Length 233;
Best Local Similarity 42.0%; Pred. No. 3.2e-31;
Matches 94; Conservative 22; Mismatches 57; Indels 51; Gaps 4;

QY 11 RALVADPVGYKLRQKGYVCGAGPBGPAADPLHQARAAAGDEPFRFRRTSDLAQQLH 39
Db 6 RALVADPVGYKLRQKGYVCGAGPBGPAADPLHQARAAAGDEPFRFRRTSDLAQQLH 65
QY 40 D-----PLHQARAAAGDEPFRFRRTSDLAQQLH 81
Db 66 NGATGSHSSSLDAREVLPMTAVKQALREAGDEFEFRFRRTSDLAQQLH 125
QY 82 VSELFGCGPVMGRVAFVFGAALCAESVKNKEMEPVGVQVDMVAVYETRLADWISS 141

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Db      126 VVNELEFRDGVNMGRIYAFPSFGALCVESVDKEMETLVRIAMATYLANDHEPVIQEN 185
Qy      142 GGAFFALYGDALAEARLR--GNMVSRTVLTGVALGAL 183
Db      186 GGMDFVELYGNNAAESRRGQERFNRWPLTGMTVAGVLLGSL 229

RESULT 12
BCLX CHICK
ID      007816; STANDARD; PRT; 229 AA.
AC      007816; Q98908;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN      Name=BCL2L1; Synonyms=BCL-X, BCLX;
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM SHORT).
RX      MEDLINE=93364977; PubMed=8358789; DOI=10.1016/0092-8674(93)90508-N;
RA      Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindersten T.,
RA      Turka L.A., Mo X., Nunez G., Thompson C.B.;
RT      "bcl-x, a bcl-2-related gene that functions as a dominant regulator of
RT      apoptotic cell death.";
RL      Cell 74:597-608(1993).
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORM LONG).
RX      STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX      MEDLINE=97264485; PubMed=9110311;
RX      DOI=10.1002/(SICI)1098-2795(199705)47:1<26::AID-MRD4>3.3.CO;2-V;
RA      Vilgrazsa X., Mezquita C., Mezquita J.;
RT      "Differential expression of bcl-2 and bcl-x during chicken
RT      spermatogenesis.";
RL      Mol. Reprod. Dev. 47:26-29(1997).
RN      [3]
RP      FUNCTION: Dominant regulator of apoptotic cell death. The long
RN      form displays cell death repressor activity, whereas the short
RN      isoform promotes apoptosis (By similarity).
CC      - SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC      envelope (By similarity).
CC      - ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=Long;
CC      IsoId=Q07816-1; Sequence=Displayed;
CC      Name=Short;
CC      IsoId=Q07816-2; Sequence=VSP_000514;
CC      - TISSUE SPECIFICITY: Highest expression in organs with lymphoid
CC      development.
CC      - DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC      function. Inactive BH1 and BH2 domains are required for anti-
CC      apoptotic activity (By similarity).
CC      - SIMILARITY: Belongs to the Bcl-2 family.
CC      - SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC      - SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC      - SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC      - SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC      - This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL, Z23110; CAAB0657.1; -
DR      EMBL, U26645; AAB07677.1; -
DR      PIR, A47537; A47537.
DR      HSSP, P53563; IAF3.

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DR      InterPro; IPR000712; Bcl2_BH.
DR      InterPro; IPR003093; Bcl2_BH4.
DR      InterPro; IPR002475; Bcl2_family.
DR      InterPro; IPR004725; Bcl2_reg.
DR      Pfam; PF00452; Bcl-2; 1.
DR      Pfam; PF02180; BH4; 1.
DR      TIGRfam; TIGR00865; bcl-2; 1.
DR      PROSITE; PS50062; BCL2_FAMILY; 1.
DR      PROSITE; PS01080; BH1; 1.
DR      PROSITE; PS01258; BH2; 1.
DR      PROSITE; PS01259; BH3; 1.
DR      PROSITE; PS01260; BH4; 1.
DR      PROSITE; PS50063; BH4_2; 1.
KW      Alternative splicing; Apoptosis; Transmembrane.
FT      DOMAIN 4
FT      DOMAIN 82 96 BH3.
FT      DOMAIN 125 144 BH1.
FT      DOMAIN 176 191 BH2.
FT      TRANSMEM 206 223 Potential.
FT      VARSPIC 185 229 ERFVLYGNNAAELEKRGQETPFKMLTGATVAGVLLGSL
FT      LSRK -> VRTALP (in isoform Short).
FT      /FTID=VSP_000514.
SQ      SEQUENCE 229 AA; 25733 MW; A97D3A4D04C0E9DA CRC64;
Query Match 42.9%; Score 432.5; DB 1; Length 229;
Best Local Similarity 41.7%; Pred. No. 1.3e-30;
Matches 95; Conservative 22; Mismatches 62; Indels 49; Gaps 4;
Qy      11 PALVADFVGYKLRQKGY-----YCGAGGEGP----- 37
Db      6 RELVDFVSYKLSQRGHCHSELEEDENRTDTAAEEMDSVLNGLSPWHPAGHYVNGAT 65
Qy      38 -----AADPLHQMARAGDEFFRRPRTSDLAQLHTPPGSAQGRFTVSD 85
Db      66 VHSSELEHETIVASDVQRQLRDAGDEFELEKRRASDLTSQHLTPGAYQSEGVN 125
Qy      86 LFGGPNWGRVAFVFGAALCAESVNMKEPLVGVQVQDMVAYLETRLADMIHSSGMA 145
Db      126 LRFHDGVNMGRIYAFPSFGALCVESVDKEMRVLVGRIVSMNTTYLTDHPITQENGW 185
Qy      146 EFRALYGDALAEARLRREGNMASVTVTLTGVALGALTVGAFFASK 193
Db      186 RFDVLYGNNA---AELRKQETPFKMLTGATVAGVLL-LGSLLSRK 229

RESULT 13
ID      Q8SQ42; PRELIMINARY; PRT; 233 AA.
AC      Q8SQ42;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Bcl-xL protein.
GN      Name=bcl-xL.
OS      Felis silvestris catus (Cat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX      NCBI_TaxID=9685;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Nagafuchi S., Sano J., Kano R., Hasegawa A.;
RL      Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR      EMBL, AB080951; BAB85856.2; -
DR      HSSP, Q07817; IMAZ.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0042981; P:regulation of apoptosis; IEA.
DR      InterPro; IPR000712; Bcl2_BH.
DR      InterPro; IPR003093; Bcl2_BH4.
DR      InterPro; IPR002475; BCL2_family.
DR      InterPro; IPR004725; Bcl2_reg.
DR      Pfam; PF00452; Bcl-2; 1.
DR      Pfam; PF02180; BH4; 1.
DR      SMART; SM00337; BCL; 1.

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DR SMART: SM0265; BH4; 1.
 DR TIGRFAMs: TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 DR SEQUENCE 233 AA; 26017 MW; CD17F24FE9D47BC9 CRC64;
 Query Match 42.8%; Score 432.5; DB 2; Length 233;
 Best Local Similarity 41.8%; Pred. No. 1.3e-30;
 Matches 97; Conservative 23; Mismatches 58; Indels 55; Gaps 5;
 QY 11 RALVADPVGKLRQKGY-----V 28
 DB 6 RELVVDPLSYLQKGYGWSRSPDVENRTPEPGTSEMETPSAINGNPSMLADSPAV 65
 QY 29 CGAGPGEGBPAD-----PLHQMRAAGDEPFRPRFRPSDLAOLHTVPGSAOQRT 80
 DB 66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFEKTRRAFSDLTSQHLITPGRAYSFE 124
 QY 81 QVSDLEFQGGPNNGRLVAFVFGAALCAESVKNKMEPLVGVQVODMVAAYLETRLADWHS 140
 DB 125 QVNVLEFRDGVNNGRIYVAFSFGALCVESVDKEMQVLVSRIAMMATYINDHLEPWIOE 184
 QY 141 SGGHAEFTALYGDALBEARLRREGNMAVSRTVLTGAVALGALTVGAFPAK 193
 DB 185 NGGWDTFVELYGNNAAESRKGERSNRWFLTGMTLAVG-VLLGSLFSRK 233
 RESULT 14
 BCLX_PIG STANDARD; PRT; 233 AA.
 AC 07773;
 DT 15-JUN-1999 (Rel. 38, Created)
 DT 15-JUN-1999 (Rel. 38, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
 GN Name=BCL2L1; Synonyms=BCLX, BCL2L;
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxId=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99171363; PubMed=10072723; DOI=10.1006/jmcc.1998.0855;
 RA Bartling B., Hoffmann J., Holte J., Schulz R., Heusch G., Dierker D.;
 RT "Quantification of cardioprotective gene expression in porcine short-term hibernating myocardium";
 RL J. Mol. Cell. Cardiol. 31:147-158(1999).
 CC -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-apoptotic activity is inhibited by association with SIVA isoform 1. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the voltage-dependent anion channel (VPAAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane.
 CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity). Isoform Bcl-X(L) binds to SIVA isoform 1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear envelope (By similarity).
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl-2 family members and for repression of cell death.
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By similarity). The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (By similarity).
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).
 CC EMBL; AJ001203; CA04597.1; -.
 DR HSSP; Q07817; IMAZ.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; Bcl2_family.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 KM Apoptosis; Mitochondrion; Transmembrane.
 FT DOMAIN 4
 FT 86 100 BH4.
 FT 129 148 BH3.
 FT 180 195 BH1.
 FT DOMAIN 180 195 BH2.
 FT TRANSMEM 210 226
 FT SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;
 Query Match 42.8%; Score 431.5; DB 1; Length 233;
 Best Local Similarity 41.8%; Pred. No. 1.6e-30;
 Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;
 QY 11 RALVADPVGKLRQKGY-----V 28
 DB 6 RELVVDPLSYLQKGYGWSQFTDVEENRTPEPGTSEMETPSAINGNPSMLADSPAV 65
 QY 29 CGAGPGEGBPAD-----PLHQMRAAGDEPFRPRFRPSDLAOLHTVPGSAOQRT 80
 DB 66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFEKTRRAFSDLTSQHLITPGRAYSFE 124
 QY 81 QVSDLEFQGGPNNGRLVAFVFGAALCAESVKNKMEPLVGVQVODMVAAYLETRLADWHS 140
 DB 125 QVNVLEFRDGVNNGRIYVAFSFGALCVESVDKEMQVLVSRIAMMATYINDHLEPWIOE 184
 QY 141 SGGHAEFTALYGDALBEARLRREGNMAVSRTVLTGAVALGALTVGAFPAK 183
 DB 185 NGGWDTFVELYGNNAAESRKGERSNRWFLTGMTLAVG-VLLGSL 229
 RESULT 15
 Q9N1A2 PRELIMINARY; PRT; 233 AA.
 ID Q9N1A2
 AC Q9N1A2
 DT 01-OCT-2000 (TrEMBL;rel. 15, Created)
 DT 01-OCT-2000 (TrEMBL;rel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBL;rel. 24, Last annotation update)
 DE Anti-apoptotic regulator Bcl-XL.
 GN Name=Bcl-XL;
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxId=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Lee T.L., Cancy J.M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF216205; AAF33212.1; -.

DR HSSP; 007817; 1R2D.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR InterPro: IPR002475; Bcl2_family.
 DR InterPro: IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BHL; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;

Query Match 42.8%; Score 431.5; DB 2; Length 233;
 Best Local Similarity 41.8%; Pred. No. 1.6e-30;
 Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

QY 11 PALVADPVGXKLRQKX-----V 28
 DB 6 RELVVDPLSYKLSQKGYNSQPTDVENRTEAPEGTESEAEIPSAINGNPSWHLADSPAV 65
 QY 29 CGAGPGEGBPAD-----PLHOAMRAAGDEFEFRFRPTPSDLAOLHVTGSGNQRF 80
 DB 66 NGA-TGHSSSLDARAVITPMAAVKQALREKRGDEFELRYRAFSDDLTSQDLHTPGTAYQSFE 124
 QY 81 QVSDLEFQGGPVGRLVAFVFGALCAESVKNKMEPLVGVQVQVDMVAVYLETRLADWIS 140
 DB 125 QVNNELFRDGVVWGRIVAFESFGALCVESVDKEMQVLVSRIATMATYINDHLEPWIOE 184
 QY 141 SGGMAEFTALYGDGALERARLRE--GNWASVRYVLTGAVNALGAL 183
 DB 185 NGGMDTFVELYGNNAAESRKQGRFRNFWFLGTMLAGVVLGSL 229

Search completed: April 10, 2005, 22:42:54
 Job time : 60 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 10, 2005, 20:12:38 ; Search time 65 Seconds
(without alignments)
1148.381 Million cell updates/sec

Title: US-09-925-674B-9
Perfect score: 1009
Sequence: 1 MATPASTPDRALVADFVGY.....LTGAVLGAULTVGAFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 1009 | 100.0 | 193 | 2 | AAV05531 Mouse Bcl |
| 2 | 1005 | 99.6 | 193 | 2 | AAW61391 Rat bcl-y |
| 3 | 1005 | 99.6 | 193 | 2 | AAW97391 The rat b |
| 4 | 1000 | 99.1 | 192 | 2 | AAW97393 Protein s |
| 5 | 1000 | 99.1 | 193 | 2 | AAV05530 Human Bcl |
| 6 | 1000 | 99.1 | 193 | 7 | ADD46742 Human Pro |
| 7 | 1000 | 99.1 | 193 | 8 | ADP88349 Human Bcl |
| 8 | 995 | 98.6 | 193 | 2 | AAW61392 Human bcl |
| 9 | 995 | 98.6 | 193 | 2 | AAW97392 The human |
| 10 | 993 | 98.4 | 193 | 2 | AAW36047 Human bcl |
| 11 | 993 | 98.4 | 193 | 2 | AAV05532 Mammalian |
| 12 | 990 | 98.1 | 192 | 2 | AAW97394 Mammalian |
| 13 | 967.5 | 95.9 | 192 | 2 | AAV05533 Mouse Bcl |
| 14 | 947 | 93.9 | 183 | 8 | ADP88350 Derivative |
| 15 | 876 | 86.8 | 168 | 8 | AAW36048 Mouse bcl |
| 16 | 814.5 | 80.7 | 190 | 5 | AAO18223 Human Bcl |
| 17 | 759 | 75.2 | 365 | 5 | AAW59884 Amino aci |
| 18 | 759 | 75.2 | 365 | 5 | ABG95556 Human nov |
| 19 | 759 | 75.2 | 365 | 7 | ABO34750 Fragment |
| 20 | 759 | 75.2 | 365 | 6 | AD123411 Novel hum |
| 21 | 759 | 75.2 | 365 | 8 | ADH74413 Human sec |
| 22 | 757.5 | 75.1 | 185 | 8 | ADH84148 Human dia |
| 23 | 457.5 | 45.3 | 179 | 8 | ADH52635 Chinese h |
| 24 | 448.5 | 44.4 | 199 | 8 | ADH52637 Chinese h |
| 25 | 441.5 | 43.8 | 219 | 8 | ADH52639 Chinese h |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 26 | 436.5 | 43.3 | 219 | 8 | ADH52641 Chinese h |
| 27 | 436.5 | 43.3 | 342 | 8 | ADQ97763 Mouse can |
| 28 | 436.5 | 42.9 | 411 | 4 | AAU00219 Bcl-XL-DT |
| 29 | 431.5 | 42.8 | 233 | 8 | ADQ80679 Porcine a |
| 30 | 430.5 | 42.7 | 237 | 5 | ADG78480 Wild type |
| 31 | 429.5 | 42.6 | 233 | 8 | ADH52633 Chinese h |
| 32 | 428.5 | 42.5 | 233 | 4 | AAW73303 Rat wild- |
| 33 | 428.5 | 42.5 | 233 | 7 | ADG62921 Rat Prote |
| 34 | 428.5 | 42.5 | 233 | 7 | ADG62491 Rat Prote |
| 35 | 428.5 | 42.5 | 233 | 8 | ADQ80678 Mouse ant |
| 36 | 427.5 | 42.4 | 233 | 2 | AAW68887 Human thy |
| 37 | 427.5 | 42.4 | 233 | 2 | AAW05821 Bcl-XL pr |
| 38 | 427.5 | 42.4 | 233 | 2 | AAW31530 Human ant |
| 39 | 427.5 | 42.4 | 233 | 3 | AAV69969 Human Bcl |
| 40 | 427.5 | 42.4 | 233 | 3 | AAW83223 Bcl-x pol |
| 41 | 427.5 | 42.4 | 233 | 4 | AAW50538 Human Bcl |
| 42 | 427.5 | 42.4 | 233 | 4 | AAW64262 Human Bcl |
| 43 | 427.5 | 42.4 | 233 | 4 | AAW47515 Protein e |
| 44 | 427.5 | 42.4 | 233 | 7 | ADG62493 Human Pro |
| 45 | 427.5 | 42.4 | 233 | 7 | ABW02410 Human bcl |

ALIGNMENTS

RESULT 1
ID AAV05531 standard; protein: 193 AA.
XX
AC AAV05531;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse Bcl-w protein essential for spermatogenesis.
XX
KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KV animal model.
XX
OS Mus sp.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX WPI; 1999-243890/20.
XX DR N-PSDB; AAX25133.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.
XX
PS Claim 2; Page 35; 52pp; English.
XX
CC The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2
CC family which is widely expressed and which is essential for
CC spermatogenesis. The invention relates generally to a method of treatment
CC and to an animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for reducing
CC fertility, by modulating spermatogenesis. An animal model carries a
CC mutation in at least one allele of the human or murine bcl-w gene (see
CC AA25132-35) or in a gene associated with bcl-w. Such animals have
CC disorganised seminiferous tubules and are substantially infertile, but
CC possess no other major abnormalities as determined by histological
CC examination. They can be used to screen for therapeutic molecules
CC including genetic sequences capable of inducing, enhancing or otherwise

CC Facilitating spermatogenesis in animals, or which can induce infertility
XX Sequence 193 AA;

Query Match 100.0%; Score 1009; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 9.3e-102;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASTPDTALVADPFVGYKLRQKGYCGAGPEGPAPADPLHQMRAAGDEFTTRRRT 60
DB 1 MATPASTPDTALVADPFVGYKLRQKGYCGAGPEGPAPADPLHQMRAAGDEFTTRRRT 60
QY 61 FSDLAQQLHTVTPGSAQGRFTQVSDLPFGGPNMGRVAFVFGAALCAESVKNEMEPVVG 120
DB 61 FSDLAQQLHTVTPGSAQGRFTQVSDLPFGGPNMGRVAFVFGAALCAESVKNEMEPVVG 120
QY 121 QVODMMVAYLETRLDWTHSSGWAFFETALYGDALBEARLRREGNWSVRYTLTGAVALL 180
DB 121 QVODMMVAYLETRLDWTHSSGWAFFETALYGDALBEARLRREGNWSVRYTLTGAVALL 180
QY 181 GALVTGAFPFASK 193
DB 181 GALVTGAFPFASK 193

RESULT 2
AAM61391
ID AAM61391 standard; protein; 193 AA.

AC AAM61391;
XX 02-OCT-1998 (first entry)
DE Rat bcl-y protein.
XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
OS Rattus sp.
XX US5789201-A.
XX 04-AUG-1998.
XX 11-FEB-1997; 97US-00798897.
XX 23-FEB-1996; 96US-0012201P.
XX (COCE-) COCENSYS INC.
XX Guastella J;
XX WPI; 1998-446079/38.
XX N-PSDB; AAV28333.
XX Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g. cancers.
XX Example; Fig 3A; 27pp; English.

XX The mammalian bcl-y protein is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired
XX Sequence 193 AA;

Query Match 99.6%; Score 1005; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 2.6e-101;

Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDTALVADPFVGYKLRQKGYCGAGPEGPAPADPLHQMRAAGDEFTTRRRT 60
DB 1 MATPASTPDTALVADPFVGYKLRQKGYCGAGPEGPAPADPLHQMRAAGDEFTTRRRT 60
QY 61 FSDLAQQLHTVTPGSAQGRFTQVSDLPFGGPNMGRVAFVFGAALCAESVKNEMEPVVG 120
DB 61 FSDLAQQLHTVTPGSAQGRFTQVSDLPFGGPNMGRVAFVFGAALCAESVKNEMEPVVG 120
QY 121 QVODMMVAYLETRLDWTHSSGWAFFETALYGDALBEARLRREGNWSVRYTLTGAVALL 180
DB 121 QVODMMVAYLETRLDWTHSSGWAFFETALYGDALBEARLRREGNWSVRYTLTGAVALL 180
QY 181 GALVTGAFPFASK 193
DB 181 GALVTGAFPFASK 193

RESULT 3
AAM97391
ID AAM97391 standard; protein; 193 AA.

AC AAM97391;
XX 20-MAY-1999 (first entry)
DE The rat bcl-y protein.
XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX Rattus sp.
XX US5883229-A.
XX 16-MAR-1999.
XX 25-NOV-1997; 97US-00978523.
XX 23-FEB-1996; 96US-0012201P.
XX 11-FEB-1997; 97US-00798897.
XX (COCE-) COCENSYS INC.
XX Guastella J;
XX WPI; 1999-214150/18.
XX N-PSDB; AAX15945.
XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death.
XX Disclosure; Col 15-18; 26pp; English.

XX The present sequence represents rat bcl-y protein (Rbcl-y). The specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis - conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended

CC period. In contrast, if they act as cell death stimulators, Bcl-1-y and
CC Hbcl-1-y may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites

XX Sequence 193 AA;

SO Query Match 99.6%; Score 1005; DB 2; Length 193;

Best Local Similarity 99.5%; Pred. No. 2.6e-101; Indels 0; Gaps 0;
Matches 192; Conservative 0; Mismatches 1;

QY 1 MATPASTPDTALVADPFGYGLRKGVCAGPGSGPADPLHQMRAAGDEFFTRFRRT 60

DB 1 MATPASTPDTALVADPFGYGLRKGVCAGPGSGPADPLHQMRAAGDEFFTRFRRT 60

QY 61 PSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNKMEPLVG 120

DB 61 PSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNKMEPLVG 120

QY 121 QVODMMVTYLETRLADWIHSSGMAEFTALYGDGALBEARLRGNMNASVRTLGAVAL 180

DB 121 QVODMMVTYLETRLADWIHSSGMAEFTALYGDGALBEARLRGNMNASVRTLGAVAL 180

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

CC with a disruption of the cell death pathway. If they act as cell death
CC inhibitors, they may be used in therapies to treat subjects suffering
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC degenerative diseases (especially multiple sclerosis), myocardial
CC infarction, vitally induced cell death, aging, spinal cord injuries and
CC amyotrophic lateral sclerosis- conditions where cells under go premature
CC cell death as a result of triggers which may or may not be apparent. They
CC may also be used in this way to develop cell lines which remain viable in
CC culture for an extended period. In contrast, if they act as cell death
CC stimulators, Bcl-1-y and Hbcl-1-y may be used to treat conditions associated
CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma
CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites

XX Sequence 192 AA;

SO Query Match 99.1%; Score 1000; DB 2; Length 192;

Best Local Similarity 99.5%; Pred. No. 8.9e-101; Indels 0; Gaps 0;
Matches 191; Conservative 0; Mismatches 1;

QY 2 ATPASTPDTALVADPFGYGLRKGVCAGPGSGPADPLHQMRAAGDEFFTRFRRT 61

DB 1 ATPASTPDTALVADPFGYGLRKGVCAGPGSGPADPLHQMRAAGDEFFTRFRRT 60

QY 62 SDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNKMEPLVG 121

DB 61 SDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNKMEPLVG 120

QY 122 VODMMVTYLETRLADWIHSSGMAEFTALYGDGALBEARLRGNMNASVRTLGAVAL 181

DB 121 VODMMVTYLETRLADWIHSSGMAEFTALYGDGALBEARLRGNMNASVRTLGAVAL 180

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

RESULT 5
ID AAY05530 standard; protein; 193 AA.

AC AAY05530;

XX 05-JUL-1999 (first entry)

DE Human Bcl-1-w protein essential for spermatogenesis.

KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;

XX animal model.

OS Homo sapiens.

XX WO9913710-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98NO-AU000764.

XX 16-SEP-1997; 97AU-00009228.

XX (HALT-) HALT INST MEDICAL RES WALTER & ELIZA.

XX WPI; 1999-243890/20.

XX N-PSDB; AAX25132.

XX An animal model exhibiting reduced levels of a Bcl-1-w protein and/or

XX protein associated with Bcl-1-w.

XX Claim 2; Page 33; 52pp; English.

XX The present sequence is human Bcl-1-w, a pro-survival member of the Bcl-2

XX The specification describes rat bcl-1-y protein (Bcl-1-y) and human bcl-1-y

XX protein (Hbcl-1-y). Bcl-1-y and Hbcl-1-y are homologues of the bcl-2 protein

XX thought to be involved in programmed cell death (apoptosis and necrosis).

XX Bcl-1-y and Hbcl-1-y proteins may be used to treat conditions associated

CC family which is widely expressed and which is essential for
CC spermatogenesis. The invention relates generally to a method of treatment
CC and to an animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for reducing
CC fertility, by modulating spermatogenesis. An animal model carries a
CC mutation is at least one allele of the human or murine bcl-w gene (see
CC AX55133-35) or in a gene associated with bcl-w. Such animals have
CC disorganised seminiferous tubules and are substantially infertile, but
CC possess no other major abnormalities as determined by histological
CC examination. They can be used to screen for therapeutic molecules
CC including genetic sequences capable of inducing, enhancing or otherwise
CC facilitating spermatogenesis in animals, or which can induce infertility
SQ Sequence 193 AA;

Query Match 99.1%; Score 1000; DB 2; Length 193;
Best Local Similarity 99.0%; Pred. No. 9e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADFGYKLRQKGYVCGAGPGEPPADPLHQMRAAGDEFETRRRT 60
DB 1 MATPASPDRALVADFGYKLRQKGYVCGAGPGEPPADPLHQMRAAGDEFETRRRT 60
QY 61 FSDLAQLHVTPTGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEPVLV 120
DB 61 FSDLAQLHVTPTGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEPVLV 120
QY 121 QVQDMWVAVLETRLADWTHSSGGMAEFTALYGDGALAEARRLRGNMVASVRTVLTGAVAL 180
DB 121 QVQDMWVAVLETRLADWTHSSGGMAEFTALYGDGALAEARRLRGNMVASVRTVLTGAVAL 180
QY 181 GALVTVGAFPPASK 193
DB 181 GALVTVGAFPPASK 193

RESULT 6
ADDA6742
ID ADD6742 standard; protein; 193 AA.
AC ADD6742;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein Q92843, SEQ ID NO 12427.

XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
FN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (PARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX DR GENBANK; Q92843.
XX

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PS Example 1; Page; 1017p; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 193 AA;
Query Match 99.1%; Score 1000; DB 7; Length 193;
Best Local Similarity 99.0%; Pred. No. 9e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADFGYKLRQKGYVCGAGPGEPPADPLHQMRAAGDEFETRRRT 60
DB 1 MATPASPDRALVADFGYKLRQKGYVCGAGPGEPPADPLHQMRAAGDEFETRRRT 60
QY 61 FSDLAQLHVTPTGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEPVLV 120
DB 61 FSDLAQLHVTPTGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEPVLV 120
QY 121 QVQDMWVAVLETRLADWTHSSGGMAEFTALYGDGALAEARRLRGNMVASVRTVLTGAVAL 180
DB 121 QVQDMWVAVLETRLADWTHSSGGMAEFTALYGDGALAEARRLRGNMVASVRTVLTGAVAL 180
QY 181 GALVTVGAFPPASK 193
DB 181 GALVTVGAFPPASK 193

RESULT 7
ADP88349
ID ADP88349 standard; protein; 193 AA.
AC ADP88349;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human Bcl-w protein.

XX Human; Bcl-w protein.
KW Bcl-w; human; protein structure; protein co-ordinate data.
KW Homo sapiens.
OS
OS WO2004050697-A1.
PN
PN 17-JUN-2004.
XX

XX 03-DEC-2003; 2003MO-AU001624.
XX
XX
XX 03-DEC-2002; 2002AU-00953259.
XX
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
XX Hinde MG, Huang DCS, Day CL;
XX WPI; 2004-487529/46.
XX
XX Solution useful for identifying or selecting agents that are capable of
XX inhibiting biological activity of Bcl-w, comprises molecule that has Bcl-
XX PT w active site defined by specific structure coordinates of Bcl-w amino
XX acid residues.
XX
XX PS Disclosure; Page 804-805; 810pp; English.
XX
XX The present invention relates to a solution comprising a molecule or
XX molecular complex that comprises at least a fragment of Bcl-w. Also
XX disclosed is the structure of Bcl-w, in the form of protein coordinate
XX data. The solution is useful for identifying, selecting or designing
XX agents that are capable of inhibiting or potentiating one or more
XX biological activity of Bcl-w, and in solving the structures of other
XX proteins with similar structure. It is also useful for characterizing the
XX three-dimensional structure of the Bcl-w molecule, molecular complex or
XX its derivative. The present sequence is the human Bcl-w protein.
XX
XX SQ Sequence 193 AA;
XX
XX Query Match 99.1%; Score 1000; DB 8; Length 193;
XX Best Local Similarity 99.0%; Pred. No. 9e-101;
XX Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MATPASTPDRALVADVFVGYKLRQKGYVCGAGPGEGBPAADPLHQAMRAAGDEFTFRRT 60
XX |
XX 1 MATPASA.PDRALVADVFVGYKLRQKGYVCGAGPGEGBPAADPLHQAMRAAGDEFTFRRT 60
XX |
XX 61 FSDLAQLHTTPGSAOQRFVDSDELFOGCPNMGRLVAFVFGAALCAESYNKMEPLVG 120
XX |
XX 61 FSDLAQLHTTPGSAOQRFVDSDELFOGCPNMGRLVAFVFGAALCAESYNKMEPLVG 120
XX |
XX 121 QVODMVAAYLETRLADWIHSSGMAEFTALYGDALBEARLRGNMNAVTVLTGAVAL 180
XX |
XX 121 QVODMVAAYLETRLADWIHSSGMAEFTALYGDALBEARLRGNMNAVTVLTGAVAL 180
XX |
XX 181 GALVTVGAFPAASK 193
XX |
XX 181 GALVTVGAFPAASK 193
XX |
XX
XX RESULT 8
XX AAW61392
XX ID AAW61392 standard; protein; 193 AA.
XX
XX AAW61392;
XX
XX 02-OCT-1998 (first entry)
XX
XX Human bcl-y protein.
XX
XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
XX
XX Homo sapiens.
XX
XX US5789201-A.
XX
XX 04-AUG-1998.
XX
XX 11-FEB-1997; 97US-00798897.
XX
XX 23-FEB-1996; 96US-0012201P.
XX

PA (COCE-) COCENSYS INC.
XX
XX Guastella J;
XX
XX WPI; 1998-446079/38.
XX
XX DR N-PSDB; AAV28334.
XX
XX Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
XX PT recombinant protein for use in treating uncontrolled cell growth e.g.
XX cancers.
XX
XX Example; Column 17/18; 27pp; English.
XX
XX The mammalian bcl-y protein is a member of the bcl-2 family, components
XX in the cell death pathway. The bcl-2 family have both apoptotic activity
XX and the apoptosis blocking activity. bcl-y falls in the apoptosis
XX activity category. The recombinant protein may be used to prevent
XX uncontrolled cell growth, either by its direct administration to
XX CC recombinant genetic constructs to increase its expression in vivo. Also,
XX antisense constructs can be used in disorders where prevention of cell
XX death is desired
XX
XX SQ Sequence 193 AA;
XX
XX Query Match 98.6%; Score 995; DB 2; Length 193;
XX Best Local Similarity 98.4%; Pred. No. 3.2e-100;
XX Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 MATPASTPDRALVADVFVGYKLRQKGYVCGAGPGEGBPAADPLHQAMRAAGDEFTFRRT 60
XX |
XX 1 MATPASA.PDRALVEDVFVGYKLRQKGYVCGAGPGEGBPAADPLHQAMRAAGDEFTFRRT 60
XX |
XX 61 FSDLAQLHTTPGSAOQRFVDSDELFOGCPNMGRLVAFVFGAALCAESYNKMEPLVG 120
XX |
XX 61 FSDLAQLHTTPGSAOQRFVDSDELFOGCPNMGRLVAFVFGAALCAESYNKMEPLVG 120
XX |
XX 121 QVODMVAAYLETRLADWIHSSGMAEFTALYGDALBEARLRGNMNAVTVLTGAVAL 180
XX |
XX 121 QVODMVAAYLETRLADWIHSSGMAEFTALYGDALBEARLRGNMNAVTVLTGAVAL 180
XX |
XX 181 GALVTVGAFPAASK 193
XX |
XX 181 GALVTVGAFPAASK 193
XX |
XX
XX RESULT 9
XX AAW97392
XX ID AAW97392 standard; protein; 193 AA.
XX
XX AAW97392;
XX
XX 20-MAY-1999 (first entry)
XX
XX The human bcl-y protein.
XX
XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Rbcl-y; bcl-2 homologue;
XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
XX multiple sclerosis; myocardial infarction; vitally induced cell death;
XX aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
XX premature cell death; cell death stimulator; prolonged cell life span;
XX Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
XX Homo sapiens.
XX
XX US5883229-A.
XX
XX 16-MAR-1999.
XX
XX 25-NOV-1997; 97US-00978523.
XX
XX 23-FEB-1996; 96US-0012201P.
XX
XX 11-FEB-1997; 97US-00798897.
XX

XX (COCE-) COCENSYS INC.
 XX Guastella J;
 PI WPI: 1999-214150/18.
 DR N-PSDB; AAX15946.
 XX Novel bcl-Y homologues of the rat and human bcl-2 protein - useful for
 PT modulating programmed cell death.
 XX Claim 1; Col 17-18; 26pp; English.
 XX The present sequence represents human bcl-Y protein (Hbcl-Y). The
 CC specification also describes rat bcl-Y protein (Rbcl-Y). Rbcl-Y and Hbcl-
 CC Y are homologues of the bcl-2 protein thought to be involved in
 CC programmed cell death (apoptosis and necrosis). Rbcl-Y and Hbcl-Y
 CC proteins may be used to treat conditions associated with a disruption of
 CC the cell death pathway. If they act as cell death inhibitors, they may be
 CC used in therapies to treat subjects suffering from: strokes, head trauma,
 CC Alzheimer's Disease, neural and muscular degenerative diseases
 CC (especially multiple sclerosis), myocardial infarction, vitally induced
 CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
 CC - conditions where cells under go premature cell death as a result of
 CC triggers which may or may not be apparent. They may also be used in this
 CC way to develop cell lines which remain viable in culture for an extended
 CC period. In contrast, if they act as cell death stimulators, Rbcl-Y and
 CC Hbcl-Y may be used to treat conditions associated with prolonged cell
 CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)
 CC and auto/hyperimmune diseases. They may also be used to cause cell death
 CC in, and hence control, parasites
 XX
 SQ Sequence 193 AA;
 Query Match 98.6%; Score 995; DB 2; Length 193;
 Best Local Similarity 98.4%; Pred. No. 3.2e-100;
 Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MATPASTPTPRALVADPFGVGYKLRQKGYVCGAGPGGPAADPLHQMRAGDEFFETRRFRT 60
 DB 1 MATPASPPTPRALVADPFGVGYKLRQKGYVCGAGPGGPAADPLHQMRAGDEFFETRRFRT 60
 QY 61 FSDLAALQHLVTPGSAQOQRTQVSDLFQGGPVMGRLVAFVFGAALCAESVNMKEPVLVG 120
 DB 61 FSDLAALQHLVTPGSAQOQRTQVSDLFQGGPVMGRLVAFVFGAALCAESVNMKEPVLVG 120
 QY 121 QVQDMNVAVLETRLDWTHSSGMAEFTALYGDGALBEARLRREGNMAVTVTLTGAVALL 180
 DB 121 QVQDMNVAVLETRLDWTHSSGMAEFTALYGDGALBEARLRREGNMAVTVTLTGAVALL 180
 QY 181 GALVTVGAFPAASK 193
 DB 181 GALVTVGAFPAASK 193
 RESULT 10
 AAW36047
 ID AAW36047 standard; protein; 193 AA.
 AC AAW36047;
 XX
 XX 22-APR-1998 (first entry)
 DE Human bcl-w protein.
 XX
 XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 KW diagnosis; degenerative disease.
 XX
 XX Homo sapiens.
 OS
 XX MO9735971-AI.
 PN
 XX 02-OCT-1997.

XX -27-MAR-1997; 97WO-AU000199.
 PF
 XX 27-MAR-1996; 96AU-00008965.
 PR
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA
 PI Cory S, Adams JM, Gibson LM, Holmgren SP;
 XX WPI: 1997-489635/45.
 DR N-PSDB; AAT96577.
 XX
 PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
 PT inhibit cell survival, e.g. for treatment of cancer and degenerative
 PT diseases.
 XX Claim 6; Page 48; 86pp; English.
 XX This sequence represents a novel human protein, bcl-w, encoded by the bcl
 CC -2 gene family and extracted from an adult brain library. This gene
 CC promotes cell survival, so its modulation is useful in treatment of
 CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
 CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
 CC ischaemia, human immunodeficiency virus infection or in cell transplants.
 CC Up-regulation of the gene can also be used to modify cell lines cultured
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
 CC and to increase survival of primary explants during genetic modification.
 CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
 CC antibody production or screening of potential modulators
 XX
 SQ Sequence 193 AA;
 Query Match 98.4%; Score 993; DB 2; Length 193;
 Best Local Similarity 97.9%; Pred. No. 5.3e-100;
 Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MATPASTPTPRALVADPFGVGYKLRQKGYVCGAGPGGPAADPLHQMRAGDEFFETRRFRT 60
 DB 1 MATPASPPTPRALVADPFGVGYKLRQKGYVCGAGPGGPAADPLHQMRAGDEFFETRRFRT 60
 QY 61 FSDLAALQHLVTPGSAQOQRTQVSDLFQGGPVMGRLVAFVFGAALCAESVNMKEPVLVG 120
 DB 61 FSDLAALQHLVTPGSAQOQRTQVSDLFQGGPVMGRLVAFVFGAALCAESVNMKEPVLVG 120
 QY 121 QVQDMNVAVLETRLDWTHSSGMAEFTALYGDGALBEARLRREGNMAVTVTLTGAVALL 180
 DB 121 QVQDMNVAVLETRLDWTHSSGMAEFTALYGDGALBEARLRREGNMAVTVTLTGAVALL 180
 QY 181 GALVTVGAFPAASK 193
 DB 181 GALVTVGAFPAASK 193
 RESULT 11
 AAY05532
 ID AAY05532 standard; protein; 193 AA.
 AC AAY05532;
 XX
 XX 05-JUL-1999 (first entry)
 DE Human Bcl-w protein essential for spermatogenesis.
 XX
 XX Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
 KW animal model.
 XX
 XX Homo sapiens.
 OS
 XX MO9913710-AI.
 PN
 XX 25-MAR-1999.
 PD
 XX 16-SEP-1998; 98MO-AU000764.

XX 16-SEP-1997; 97AU-00009228.
 PR (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA Cory S, Adams J, Print C, Gibson L, Koentgen F;
 XX WPI: 1999-243890/20.
 DR N-PSDB; AAX25134.
 XX
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 XX
 PS Disclosure; Page 37; 52pp; English.
 XX
 CC The present sequence is described of a derivative of human Bcl-w (see
 CC also AAY05530), a pro-survival member of the Bcl-2 family that is widely
 CC expressed and which is essential for spermatogenesis. The invention
 CC relates generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation is at least one
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
 CC associated with bcl-w. Such animals have disorganised seminiferous tubules
 CC and are substantially infertile, but possess no other major abnormalities
 CC as determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility
 XX
 SQ Sequence 193 AA;

Query Match 98.4%; Score 993; DB 2; Length 193;
 Best Local Similarity 97.9%; Pred. No. 5.3e-100; Indels 0; Gaps 0;
 Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASPPDTRALVADPFVGYLRQKGYVCGAPGPGPADPLHQMRAAGDEFETRFRPT 60
 DB 1 MATPASAPDTRALVADPFVGYLRQKGYVCGAPGPGPADPLHQMRAAGDEFETRFRPT 60
 QY 61 FSDLAALQHTVTPGSAQOQRTQVSDLPFGCGPNMGLVAFVFGALCAESVNMKEPVLVG 120
 DB 61 FSDLAALQHTVTPGSAQOQRTQVSDLPFGCGPNMGLVAFVFGALCAESVNMKEPVLVG 120
 QY 121 QVDMWVAVYLETRLADWTHSSGNAEFYALYGDGALBEARRLREGNMASVRTVLGAVALG 180
 DB 121 QVDMWVAVYLETRLADWTHSSGNAEFYALYGDGALBEARRLREGNMASVRTVLGAVALG 180
 QY 181 GALVTGAFPAK 193
 DB 181 GALVTGAFPAK 193

RESULT 12
 AAW97394
 ID AAW97394 standard; protein: 192 AA.

XX AAW97394;
 AC
 XX 20-MAY-1999 (first entry)
 DT
 XX Mammalian bcl-y protein.
 DE
 XX Rat bcl-y protein; Bcl-y; human bcl-y protein; Bcl-y; bcl-2 homologue;
 KM programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KM head trauma; Alzheimer's disease; neural; muscular degenerative disease;
 KM multiple sclerosis; myocardial infarction; vitally induced cell death;
 KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KM premature cell death; cell death stimulator; prolonged cell life span;
 KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
 XX
 OS Mammalia.

XX US5883229-A.
 PN 16-MAR-1999.
 PD 25-NOV-1997; 97US-00978523.
 XX 23-FEB-1996; 96US-0012201P.
 PR 11-FEB-1997; 97US-00798897.
 XX (COCE-) COCENSYS INC.
 PA Guastella J;
 XX WPI: 1999-214150/18.
 DR
 XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
 PT modulating programmed cell death.
 PT
 PS Claim 2; Col 19-22; 26pp; English.

XX The present sequence represents a mammalian bcl-y protein. The
 CC specification describes rat bcl-y protein (Bcl-y) and human bcl-y
 CC protein (Hbcl-y). Bcl-y and Hbcl-y are homologues of the bcl-2 protein
 CC thought to be involved in programmed cell death (apoptosis and necrosis).
 CC Bcl-y and Hbcl-y proteins may be used to treat conditions associated
 CC with a disruption of the cell death pathway. If they act as cell death
 CC inhibitors, they may be used in therapies to treat subjects suffering
 CC from: strokes, head trauma, Alzheimer's disease, neural and muscular
 CC degenerative diseases (especially multiple sclerosis), myocardial
 CC infarction, vitally induced cell death, aging, spinal cord injuries and
 CC amyotrophic lateral sclerosis - conditions where cells under go premature
 CC cell death as a result of triggers which may or may not be apparent. They
 CC may also be used in this way to develop cell lines which remain viable in
 CC culture for an extended period. In contrast, if they act as cell death
 CC stimulators, Bcl-y and Hbcl-y may be used to treat conditions associated
 CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma
 CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites

Query Match 98.1%; Score 990; DB 2; Length 192;
 Best Local Similarity 98.4%; Pred. No. 1.1e-99; Indels 0; Gaps 0;
 Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASTDTRALVADPFVGYLRQKGYVCGAPGPGPADPLHQMRAAGDEFETRFRPT 61
 DB 1 ATPASAPDTRALVADPFVGYLRQKGYVCGAPGPGPADPLHQMRAAGDEFETRFRPT 60
 QY 62 SDLAALQHTVTPGSAQOQRTQVSDLPFGCGPNMGLVAFVFGALCAESVNMKEPVLVG 121
 DB 61 SDLAALQHTVTPGSAQOQRTQVSDLPFGCGPNMGLVAFVFGALCAESVNMKEPVLVG 120
 QY 122 QVDMWVAVYLETRLADWTHSSGNAEFYALYGDGALBEARRLREGNMASVRTVLGAVALG 181
 DB 121 QVDMWVAVYLETRLADWTHSSGNAEFYALYGDGALBEARRLREGNMASVRTVLGAVALG 180
 QY 182 ALVTGAFPAK 193
 DB 181 ALVTGAFPAK 192

RESULT 13
 AAY05533
 ID AAY05533 standard; protein: 192 AA.

XX AAY05533;
 AC
 XX 05-JUN-1999 (first entry)
 DT
 XX Mouse Bcl-w protein derivative.
 DE
 XX

KW Spermatozoogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
 XX animal model.
 OS Mus sp.
 XX MO913710-A1.
 XX 25-MAR-1999.
 XX 16-SEP-1998; 98WO-AU000764.
 XX 16-SEP-1997; 97AU-00009228.
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX Cory S, Adams J, Print C, Gibson L, Koentgen F;
 DR WPI; 1999-243890/20.
 DR N-PSDB; AAX25135.
 XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 XX Disclosure; Page 39; 52pp; English.
 PS The present sequence is described of a derivative of mouse Bcl-w (see
 CC also AAY05531), a pro-survival member of the Bcl-2 family that is widely
 CC expressed and which is essential for spermatogenesis. The derivative
 CC lacks the 24 N-terminal amino acids of Bcl-w. The invention relates
 CC generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation is at least one
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
 CC associated with bcl-w. Such animals have disorganised seminiferous tubules
 CC and are substantially infertile, but possess no other major abnormalities
 CC as determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility
 XX
 SQ Sequence 192 AA;
 Query Match 95.9%; Score 967.5; DB 2; Length 192;
 Best Local Similarity 95.9%; Pred. No. 3.2e-97;
 Matches 185; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
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 DB 1 MPTPASTPTPTALVADPFVGYLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETFRRT 60
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 DB 121 QVODMVAVYLETPLADWTHSSGWAFFTAALYGDALBEARLRREGNVAASVRLTGAVAL 180
 QY 181 GALVTGAFPAASK 193
 DB 180 GALVTGAFPAASK 192
 RESULT 14
 ADP88350
 ID ADP88350 standard; protein; 183 AA.
 XX
 AC ADP88350;
 XX
 DT 09-SEP-2004 (first entry)

DE Derivative of human Bcl-w protein.
 XX
 KW Bcl-w; human; protein structure; protein co-ordinate data; mutant;
 XX mutein.
 OS Homo sapiens.
 XX Synthetic.
 XX Key location/Qualifiers
 FT Misc-difference 128 /note="wild-type Ala substituted by Glu"
 FT
 XX WO2004050697-A1.
 XX 17-JUN-2004.
 XX 03-DEC-2003; 2003WO-AU001624.
 XX 03-DEC-2002; 2002AU-00953259.
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX Hinds MG, Huang DCS, Day CL;
 XX WPI; 2004-487529/46.
 DR
 XX
 XX Solution useful for identifying or selecting agents that are capable of
 PT inhibiting biological activity of Bcl-w, comprises molecule that has Bcl-
 PT w active site defined by specific structure coordinates of Bcl-w amino
 PT acid residues.
 XX
 PS Claim 16; Page 805-806; 810pp; English.
 XX
 CC The present invention relates to a solution comprising a molecule or
 CC molecular complex that comprises at least a fragment of Bcl-w. Also
 CC disclosed is the structure of Bcl-w, in the form of protein coordinate
 CC data. The solution is useful for identifying, selecting or designing
 CC agents that are capable of inhibiting or potentiating one or more
 CC biological activity of Bcl-w, and in solving the structures of other
 CC proteins with similar structure. It is also useful for characterizing the
 CC three-dimensional structure of the Bcl-w molecule, molecular complex or
 CC its derivative. The present sequence is a derivative of the human Bcl-w
 CC protein.
 CC
 SQ Sequence 183 AA;
 Query Match 93.9%; Score 947; DB 8; Length 183;
 Best Local Similarity 98.4%; Pred. No. 5.3e-95;
 Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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 DB 1 MATPASTPTPTALVADPFVGYLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETFRRT 60
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 QY 121 QVODMVAVYLETPLADWTHSSGWAFFTAALYGDALBEARLRREGNVAASVRLTGAVAL 180
 DB 121 QVODMVAVYLETPLADWTHSSGWAFFTAALYGDALBEARLRREGNVAASVRLTGAVAL 180
 QY 181 GAL 183
 DB 181 GAL 183
 RESULT 15
 AAM36048
 ID AAM36048 standard; protein; 168 AA.
 XX
 AC AAM36048;
 XX

DT 22-APR-1998 (first entry)

XX Mouse bcl-w protein.

XX Bcl-w; Apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease.

XX Mus ap.

XX MO9735971-A1.

XX 02-OCT-1997.

XX 27-MAR-1997; 97WO-AU000199.

XX 27-MAR-1996; 96AU-00008965.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Cory S, Adams JM, Gibson LM, Holmgren SP;

XX WPI; 1997-489635/45.

XX N-PSDB; AAT96578.

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
inhibit cell survival, e.g. for treatment of cancer and degenerative
diseases.

PS Claim 6; Page 50-51; 86pp; English.

CC This sequence represents a novel protein, bcl-w, encoded by the mouse bcl
-2 gene family. This gene promotes cell survival, so its modulation is
useful in treatment of cancer or auto-immune diseases, degenerative
diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular
degeneration, hypoxia, ischaemia, human immunodeficiency virus infection
or in cell transplants. Up-regulation of the gene can also be used to
modify cell lines cultured in vivo, e.g. to develop new lines, to
facilitate isolation of hybridomas and to increase survival of primary
explants during genetic modification. It can be used to produce
recombinant Bcl-w for therapy, diagnosis, antibody production or
screening of potential modulators

SQ Sequence 168 AA;

Query Match 86.8%; Score 876; DB 2; Length 168;

Best Local Similarity 97.0%; Pred. No. 2.8e-87;

Matches 163; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MPTPASTPDRALVADVFVGYKLRQGYVCGAGPGEPPADPLHOAMRAAGDEFTRFRRT 60

QY 61 FSDLAAGLHVTTPGSAQGRFTQVSDELFOGQGNMGRLVAFVFGAALCAESVYKMEPLVG 120

DB 61 FSDLAAGLHVTTPGSAQGRFTQVSDELFOGQGNMGRLVAFVFGAALCAESVYKMEPLVG 120

QY 121 QVQDMWVAVYETRLADWVHSSGWAERTALYGDALBEARRLRGNWA 168

DB 121 QVQDMWVAVYETRLADWVHSSGWAERTALYGDALBEARRLRGNWA 168

Search completed: April 10, 2005, 22:40:50

Job time : 66 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 10, 2005, 22:43:04 ; Search time 227.5 Seconds

(without alignments)
281.650 Million cell updates/sec

Title: US-09-925-674B-9

Perfect score: 1009
Sequence: 1 MATPASTPDRALVADPVG.....LTGAVLGVTVGAFPRASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 1006 | 99.7 | 193 | 9 | US-09-925-674A-9 |
| 2 | 1000 | 99.1 | 193 | 9 | US-09-925-674A-7 |
| 3 | 1000 | 99.1 | 193 | 16 | US-10-450-366-6 |
| 4 | 759 | 75.2 | 365 | 10 | US-09-809-391-696 |
| 5 | 759 | 75.2 | 365 | 10 | US-09-882-171-696 |
| 6 | 759 | 75.2 | 365 | 15 | US-10-164-861-696 |
| 7 | 631.5 | 62.6 | 228 | 16 | US-10-659-705-2 |
| 8 | 457.5 | 45.3 | 179 | 15 | US-10-402-017-6 |
| 9 | 448.5 | 44.4 | 199 | 15 | US-10-402-017-8 |
| 10 | 441.5 | 43.8 | 219 | 15 | US-10-402-017-10 |
| 11 | 436.5 | 43.3 | 219 | 15 | US-10-402-017-12 |
| 12 | 432.5 | 42.9 | 229 | 16 | US-10-659-705-7 |
| 13 | 432.5 | 42.9 | 411 | 16 | US-10-792-517-2 |

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| 14 | 429.5 | 42.6 | 233 | 15 | US-10-402-017-4 | Sequence 4, Appl1 |
| 15 | 427.5 | 42.4 | 233 | 9 | US-09-734-846-2 | Sequence 2, Appl1 |
| 16 | 427.5 | 42.4 | 233 | 9 | US-09-952-278-6 | Sequence 6, Appl1 |
| 17 | 427.5 | 42.4 | 233 | 14 | US-10-101-482-14 | Sequence 14, Appl1 |
| 18 | 427.5 | 42.4 | 233 | 14 | US-10-072-830-4 | Sequence 4, Appl1 |
| 19 | 427.5 | 42.4 | 233 | 14 | US-10-169-223-10 | Sequence 10, Appl1 |
| 20 | 427.5 | 42.4 | 233 | 14 | US-10-302-262-2 | Sequence 2, Appl1 |
| 21 | 427.5 | 42.4 | 233 | 15 | US-10-116-275-171 | Sequence 171, Appl1 |
| 22 | 427.5 | 42.4 | 233 | 16 | US-10-450-366-5 | Sequence 5, Appl1 |
| 23 | 427.5 | 42.4 | 233 | 16 | US-10-659-705-8 | Sequence 8, Appl1 |
| 24 | 415.5 | 41.2 | 239 | 15 | US-10-148-953A-3 | Sequence 3, Appl1 |
| 25 | 414.5 | 41.1 | 152 | 14 | US-10-158-769-2 | Sequence 2, Appl1 |
| 26 | 414.5 | 41.1 | 233 | 16 | US-10-659-705-3 | Sequence 3, Appl1 |
| 27 | 412 | 40.8 | 236 | 13 | US-10-087-192-1953 | Sequence 1953, Appl1 |
| 28 | 411.5 | 40.8 | 239 | 14 | US-10-277-693A-10 | Sequence 10, Appl1 |
| 29 | 411.5 | 40.8 | 239 | 15 | US-10-003-632C-10 | Sequence 10, Appl1 |
| 30 | 411.5 | 40.8 | 239 | 15 | US-10-003-632C-13 | Sequence 13, Appl1 |
| 31 | 409.5 | 40.6 | 239 | 8 | US-08-726-211-5 | Sequence 5, Appl1 |
| 32 | 409.5 | 40.6 | 239 | 10 | US-09-993-420A-8 | Sequence 8, Appl1 |
| 33 | 409.5 | 40.6 | 239 | 14 | US-10-101-482-12 | Sequence 12, Appl1 |
| 34 | 409.5 | 40.6 | 239 | 14 | US-10-072-830-2 | Sequence 2, Appl1 |
| 35 | 409.5 | 40.6 | 239 | 14 | US-10-141-618-12 | Sequence 12, Appl1 |
| 36 | 409.5 | 40.6 | 239 | 14 | US-10-053-645A-21 | Sequence 21, Appl1 |
| 37 | 409.5 | 40.6 | 239 | 15 | US-10-387-961A-5 | Sequence 5, Appl1 |
| 38 | 409.5 | 40.6 | 239 | 15 | US-10-003-632C-1 | Sequence 1, Appl1 |
| 39 | 409.5 | 40.6 | 239 | 15 | US-10-003-632C-3 | Sequence 3, Appl1 |
| 40 | 409.5 | 40.6 | 239 | 15 | US-10-148-953A-1 | Sequence 1, Appl1 |
| 41 | 409.5 | 40.6 | 239 | 15 | US-10-148-953A-2 | Sequence 2, Appl1 |
| 42 | 409.5 | 40.6 | 239 | 16 | US-10-297-321-2 | Sequence 2, Appl1 |
| 43 | 409.5 | 40.6 | 239 | 15 | US-10-450-366-4 | Sequence 4, Appl1 |
| 44 | 409.5 | 40.6 | 239 | 16 | US-10-770-668-16 | Sequence 16, Appl1 |
| 45 | 409.5 | 40.6 | 485 | 16 | US-10-792-517-8 | Sequence 8, Appl1 |

ALIGNMENTS

RESULT 1
US-09-925-674A-9
Sequence 9, Application US/09925674A
Patent No. US20020119943A1
GENERAL INFORMATION:
APPLICANT: AMRAD Operations Pty Ltd
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
TITLE OR INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
FILE REFERENCE: 11686a
CURRENT APPLICATION NUMBER: US/09/925,674A
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/925,674
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: P8965
PRIOR FILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentm Ver. 2.1
SEQ ID NO 9
LENGTH: 193
TYPE: PRT
ORGANISM: Mouse
US-09-925-674A-9

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Best Local Similarity 99.5% Pred. No. 1.2e-96;
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 121 QVQDMWVAVLETRLDWTHSSGMAEFTALYGDALBEARLRREGNMAVSRTVLTGAVAL 180
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RESULT 2

US-09-925-674A-7
 ; Sequence 7, Application US/09925674A
 ; Patent No. US20020119943A1
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 ; APPLICANT: AMRAD Operations Pty Ltd
 ; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-1, BELONGS TO THE bcl-2
 ; FILE REFERENCE: 116864
 ; CURRENT APPLICATION NUMBER: US/09/925,674A
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 09/925,674
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: P8965
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: HUMAN
 ; US-09-925-674A-7

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 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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 Db 181 GALVTGAFPAASK 193

RESULT 3

US-10-450-366-6
 ; Sequence 6, Application US/10450366
 ; Publication No. US20040115667A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoffmann, Jörg
 ; TITLE OF INVENTION: DNA-Sequences, Which Code For An Apoptosis Signal Transduction Pr
 ; FILE REFERENCE: 1143673
 ; CURRENT APPLICATION NUMBER: US/10/450,366
 ; PRIOR FILING DATE: 2003-11-21
 ; PRIOR APPLICATION NUMBER: PCT/EP01/14597
 ; PRIOR FILING DATE: 2001-12-12
 ; PRIOR APPLICATION NUMBER: DE 100 61 766.2
 ; PRIOR FILING DATE: 2000-12-12
 ; PRIOR APPLICATION NUMBER: DE 101 00 280.7
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 193

TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Human Bcl-1-W
 US-10-450-366-6

Query Match
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 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 4

US-09-809-391-696
 ; Sequence 696, Application US/09809391
 ; Publication No. US20030049618A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: P2002P2
 ; CURRENT APPLICATION NUMBER: US/09/809,391
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 761
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 696
 ; LENGTH: 365
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-809-391-696

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RESULT 5

US-09-882-171-696
 ; Sequence 696, Application US/09882171
 ; Publication No. US20030175858A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: P2002P2
 ; CURRENT APPLICATION NUMBER: US/09/882,171
 ; CURRENT FILING DATE: 2001-06-18

Page 3

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|----|-------|---------------------|--------------|
| 1 | PRIOR | FILING DATE: | 1997-04-11 |
| 2 | PRIOR | APPLICATION NUMBER: | 60/043, 6711 |
| 3 | PRIOR | FILING DATE: | 1997-04-11 |
| 4 | PRIOR | APPLICATION NUMBER: | 60/043, 6744 |
| 5 | PRIOR | FILING DATE: | 1997-04-11 |
| 6 | PRIOR | APPLICATION NUMBER: | 60/043, 6658 |
| 7 | PRIOR | FILING DATE: | 1997-04-11 |
| 8 | PRIOR | APPLICATION NUMBER: | 60/043, 3122 |
| 9 | PRIOR | FILING DATE: | 1997-04-11 |
| 10 | PRIOR | APPLICATION NUMBER: | 60/043, 3133 |
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| 13 | PRIOR | FILING DATE: | 1997-04-11 |
| 14 | PRIOR | APPLICATION NUMBER: | 60/043, 3155 |
| 15 | PRIOR | FILING DATE: | 1997-04-11 |
| 16 | PRIOR | APPLICATION NUMBER: | 60/048, 9744 |
| 17 | PRIOR | FILING DATE: | 1997-06-06 |
| 18 | PRIOR | APPLICATION NUMBER: | 60/056, 8866 |
| 19 | PRIOR | FILING DATE: | 1997-08-22 |
| 20 | PRIOR | APPLICATION NUMBER: | 60/056, 8777 |
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| 22 | PRIOR | APPLICATION NUMBER: | 60/056, 8899 |
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| 24 | PRIOR | APPLICATION NUMBER: | 60/056, 8933 |
| 25 | PRIOR | FILING DATE: | 1997-08-22 |
| 26 | PRIOR | APPLICATION NUMBER: | 60/056, 6300 |
| 27 | PRIOR | FILING DATE: | 1997-08-22 |
| 28 | PRIOR | APPLICATION NUMBER: | 60/056, 8788 |
| 29 | PRIOR | FILING DATE: | 1997-08-22 |
| 30 | PRIOR | APPLICATION NUMBER: | 60/056, 8822 |
| 31 | PRIOR | FILING DATE: | 1997-08-22 |
| 32 | PRIOR | APPLICATION NUMBER: | 60/056, 6622 |
| 33 | PRIOR | FILING DATE: | 1997-08-22 |
| 34 | PRIOR | APPLICATION NUMBER: | 60/056, 8722 |
| 35 | PRIOR | FILING DATE: | 1997-08-22 |
| 36 | PRIOR | APPLICATION NUMBER: | 60/056, 8888 |
| 37 | PRIOR | FILING DATE: | 1997-08-22 |
| 38 | PRIOR | APPLICATION NUMBER: | 60/056, 8944 |
| 39 | PRIOR | FILING DATE: | 1997-08-22 |
| 40 | PRIOR | APPLICATION NUMBER: | 60/056, 9111 |
| 41 | PRIOR | FILING DATE: | 1997-08-22 |
| 42 | PRIOR | APPLICATION NUMBER: | 60/056, 6366 |
| 43 | PRIOR | FILING DATE: | 1997-08-22 |
| 44 | PRIOR | APPLICATION NUMBER: | 60/056, 8744 |
| 45 | PRIOR | FILING DATE: | 1997-08-22 |
| 46 | PRIOR | APPLICATION NUMBER: | 60/056, 9100 |
| 47 | PRIOR | FILING DATE: | 1997-08-22 |
| 48 | PRIOR | APPLICATION NUMBER: | 60/056, 8644 |
| 49 | PRIOR | FILING DATE: | 1997-08-22 |
| 50 | PRIOR | APPLICATION NUMBER: | 60/056, 6311 |
| 51 | PRIOR | FILING DATE: | 1997-08-22 |
| 52 | PRIOR | APPLICATION NUMBER: | 60/056, 8455 |
| 53 | PRIOR | FILING DATE: | 1997-08-22 |
| 54 | PRIOR | APPLICATION NUMBER: | 60/056, 8922 |
| 55 | PRIOR | FILING DATE: | 1997-08-22 |
| 56 | PRIOR | APPLICATION NUMBER: | 60/057, 7611 |
| 57 | PRIOR | FILING DATE: | 1997-08-22 |
| 58 | PRIOR | APPLICATION NUMBER: | 60/047, 5555 |
| 59 | PRIOR | FILING DATE: | 1997-05-23 |
| 60 | PRIOR | APPLICATION NUMBER: | 60/047, 5599 |
| 61 | PRIOR | FILING DATE: | 1997-05-23 |
| 62 | PRIOR | APPLICATION NUMBER: | 60/047, 5888 |
| 63 | PRIOR | FILING DATE: | 1997-05-23 |
| 64 | PRIOR | APPLICATION NUMBER: | 60/047, 5855 |
| 65 | PRIOR | FILING DATE: | 1997-05-23 |

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; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

```

```

Query Match 75.2%; Score 759; DB 10; Length 365;
Best Local Similarity 98.6%; Pred. No. 1.7e-70;
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 MATPASTDTRALVADPVGKLRQKGYCGAGPGEPAADPLHQAAMRAAGDEFETFRRT 60
Db 1 MATPASADTRALVADPVGKLRQKGYCGAGPGEPAADPLHQAAMRAAGDEFETFRRT 60
Qy 61 FSDLAQLHTVTPGSAQORFTQVSDDELFOGSPNMGRLVAFVFGAALCAESVKNEMELV 120
Db 61 FSDLAQLHTVTPGSAQORFTQVSDDELFOGSPNMGRLVAFVFGAALCAESVKNEMELV 120
Qy 121 QVQDMWVAIYLETRLADWIHSSG 144
Db 121 QVQDMWVAIYLETRLADWIHSSG 144

```

```

RESULT 6
US-10-164-861-696
; Sequence 696; Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861

```

```

; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-861-696

```

```

Query Match 75.2%; Score 759; DB 15; Length 365;
Best Local Similarity 98.6%; Pred. No. 1.7e-70;
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 MATPASTDTRALVADPVGKLRQKGYCGAGPGEPAADPLHQAAMRAAGDEFETFRRT 60
Db 1 MATPASADTRALVADPVGKLRQKGYCGAGPGEPAADPLHQAAMRAAGDEFETFRRT 60
Qy 61 FSDLAQLHTVTPGSAQORFTQVSDDELFOGSPNMGRLVAFVFGAALCAESVKNEMELV 120
Db 61 FSDLAQLHTVTPGSAQORFTQVSDDELFOGSPNMGRLVAFVFGAALCAESVKNEMELV 120
Qy 121 QVQDMWVAIYLETRLADWIHSSG 144
Db 121 QVQDMWVAIYLETRLADWIHSSG 144

```

```

RESULT 7
US-10-659-705-2
; Sequence 2; Application US/10659705
; Publication No. US20040117867A1
; GENERAL INFORMATION:
; APPLICANT: Look, A. Thomas
; TITLE OF INVENTION: Transgenic Cancer Models in Fish
; FILE REFERENCE: 112706.123
; CURRENT APPLICATION NUMBER: US/10/659,705
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/409,585
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BCL2 proteins
US-10-659-705-2

```

```

Query Match 62.6%; Score 631.5; DB 16; Length 228;
Best Local Similarity 67.4%; Pred. No. 1.9e-57;
Matches 124; Conservative 20; Mismatches 37; Indels 3; Gaps 1;

```

```

Qy 10 TRALVADPVGKLRQKGYCGAGPGEPAADPLHQAAMRAAGDEFETFRRTFSDLAQLH 69
Db 48 SRALVEDLVRYKLCORSLV---PEPSGAASCALHSNRAADDEFEERPROAFSISIQIH 104
Qy 70 VTPGSAQORFTQVSDDELFOGSPNMGRLVAFVFGAALCAESVKNEMELVGOVQDMWVAI 129
Db 105 VTPGTAVARFAVAGSLFQGGVNNGRIVAFVFGAALCAESVKNEMELVPRIIDMNVVY 164
Qy 130 LETRLADWIHSSGMAETALYDGALEBARREBNWASVRYTLGAVAGALVTYGAF 189
Db 165 LETNIDRWIQSGNMGRLTLTGDAIEBARROREBNWASIKTVLTGAVAGALMTVGAL 224
Qy 190 FASK 193
Db 225 FASK 228

```

```
RESULT 8
US-10-402-017-6
; Sequence 6, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; TITLE OF INVENTION: such cells
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; PRIOR APPLICATION NUMBER: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del126-83)
US-10-402-017-6

Query Match      45.3%; Score 457.5; DB 15; Length 179;
Best Local Similarity 52.0%; Pred. No. 2e-39;
Matches 91; Conservative 21; Mismatches 56; Indels 7; Gaps 2;

Qy 11 PALVADPVGKYLROKGYVCGAGPGEPAADPLHQAAMRAAGDEFTRPRTSDLAQLHV 70
Db 6 RELVVDPLSYKLSQKGYSMASAA-----AAAVKQALREAGDEFELRRARFSDLTSLQHI 60

Qy 71 TPQSAQGRFTQVSEPLFQGGPNMGRVLVAFVFGALCAESYKMEPLVGVQDMMVAYL 130
Db 61 TPGFAYQSFEGVYVELFRDGVNMGRIVAFSFGALCVESYDKEMQVLSRIASGMATYL 120

Qy 131 ETRLADHHSQGAFFALYGDGALREARLR--GNWASVRYVLGAVLAL 183
Db 121 NDHLEPFIQDNGMDTVLVELYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSL 175

RESULT 9
US-10-402-017-8
; Sequence 8, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; TITLE OF INVENTION: such cells
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; PRIOR APPLICATION NUMBER: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del146-83)
US-10-402-017-8

Query Match      44.4%; Score 448.5; DB 15; Length 199;
Best Local Similarity 47.9%; Pred. No. 2e-38;
Matches 91; Conservative 21; Mismatches 61; Indels 17; Gaps 2;

Qy 11 PALVADPVGKYLROKGYV-----GAGBGSPPADPLHQAAMRAAGDEFET 55
Db 6 RELVVDPLSYKLSQKGYSMQFSQFSDVEENRTAEAPGTSERRAAAVKQALREAGDEFEL 65

Qy 56 RFRRTFSDLAQLHVITGSAQGRFTQVSDLEFGGPNMGRVLVAFVFGALCAESYKEM 115
```

```
Db 66 RYRRAFDLTSQHLITGTAYQSEGVNLEFRDGVNMGRIVAFSFGALCVESYDKEM 125
Qy 116 EPLVGVQDMMVAYLETRLADHHSQGAFFALYDGLAEARLR--GNWASRYV 173
Db 126 QVAVSRIASMMATYLDNHLEPFIQDNGMDTVLVELYGNNAAESRKQGRFNRWFLTGMT 185

Qy 174 LTGAVLAL 183
Db 186 VAGVLLGSL 195

RESULT 10
US-10-402-017-10
; Sequence 10, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; TITLE OF INVENTION: such cells
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; PRIOR APPLICATION NUMBER: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del166-83)
US-10-402-017-10

Query Match      43.8%; Score 441.5; DB 15; Length 219;
Best Local Similarity 43.3%; Pred. No. 1.2e-37;
Matches 91; Conservative 21; Mismatches 61; Indels 37; Gaps 2;

Qy 11 PALVADPVGKYLROKGYV-----CGAGPGE 35
Db 6 RELVVDPLSYKLSQKGYSMQFSQFSDVEENRTAEAPGTSERRPESAINGNPSMHLADSPAV 65

Qy 36 GPAAADPLHQAAMRAAGDEFTRPRTSDLAQLHVPGSAQGRFTQVSDLEFGGPNMGR 95
Db 66 AAAAAYKQALREAGDEFELRRARFSDLTSLQHLITGTAYQSEGVNLEFRDGVNMGRI 125

Qy 96 LVAFVFGALCAESYKMEPLVGVQDMMVAYLETRLADHHSQGAFFALYDGA 155
Db 126 IVAFSFGALCVESYDKEMQVLSRIASMMATYLDNHLEPFIQDNGMDTVLVELYGNNA 185

Qy 156 LBEARLR--GNWASVRYVLGAVLAL 183
Db 186 AASRKQGRFNRWFLTGMTVAGVLLGSL 215

RESULT 11
US-10-402-017-12
; Sequence 12, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; TITLE OF INVENTION: such cells
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; PRIOR APPLICATION NUMBER: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 219
```

```
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del26-83)
US-10-402-017-12
```

```
Query Match
Best Local Similarity 43.3%; Score 436.5; DB 15; Length 219;
Matches 93; Conservative 22; Mismatches 57; Indels 39; Gaps 4;
```

```
QY 11 RALVADPFGYKLRQKGY-----VCGAGPGEGRPAD-- 40
DB 6 RELVDFLSYKLSQKGYSMQSPDSVDEENRTPEAGTESERAAAAYVGA-TGHSSTLDAR 64
QY 41 -----PLHQAMRAAGDEFETFRRTSPDLAOLAHYPPGSAOQRTQVSDLEFOGGEPMNG 94
DB 65 EVIPMAAVKQALREAGDEFEIKRYRAPSDLTSQHLITPGTAQYSPFEQVNVLEFRDGVNMG 124
QY 95 RLVAFFPFGAALCAESVYKEMEPVGVQVODMVAYLETRRLADWIHSSGGAFFETALYGDG 154
DB 125 RIVAFSFRGALCVESVDKEMQVLSRIASMMATYLDNDLEPWIQDNGMDTVELYGN 184
QY 155 ALPEARLRRE--GNWASVRYTLTGAVALGAL 183
DB 185 AAASRKQGERFRNFWLTGMTVAGVLLGSL 215
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RESULT 12
US-10-659-705-7
/ Sequence 7, Application US/10659705
/ Publication No. US20040117867A1
/ GENERAL INFORMATION:
/ APPLICANT: Look, A. Thomas
/ APPLICANT: Langenau, David M.
/ TITLE OF INVENTION: Transgenic Cancer Models in Fish
/ FILE REFERENCE: 112706.123
/ CURRENT APPLICATION NUMBER: US/10/659,705
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 60/409,585
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 229
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: BCL2 proteins
US-10-659-705-7
```

```
Query Match
Best Local Similarity 41.7%; Pred. No. 1,1e-36;
Matches 95; Conservative 22; Mismatches 62; Indels 49; Gaps 4;
```

```
QY 11 RALVADPFGYKLRQKGY-----VCGAGPGEGR----- 37
DB 6 RELVDFLSYKLSQKGYSMQSPDSVDEENRTPEAGTESERAAAAYVGA-TGHSSTLDAR 64
QY 38 -----AADPLHQAMRAAGDEFETFRRTSPDLAOLAHYPPGSAOQRTQVSDLEFOGGEPMNG 94
DB 66 VHRSLLEHETVRSADVQALRDAGDEFEIKRYRAPSDLTSQHLITPGTAQYSPFEQVNVLEFRDGVNMG 124
QY 86 LFOGPPMNGRLVAFVFGAALCAESVYKEMEPVGVQVODMVAYLETRRLADWIHSSGGAFFETALYGDG 154
DB 126 LFHGVNMGRIIVAFSFRGALCVESVDKEMQVLSRIASMMATYLDNDLEPWIQDNGMDTVELYGN 184
QY 146 EFTALYGGALAEERRLREGNMAVRYTLTGAVALGALVTVGAFFPASK 193
DB 186 RFLVDLYGNNA--AAELRKQGETFNNKLLTGATVAGVLL-LGSLLSRK 229
```

```
RESULT 13
US-10-792-517-2
```

```
/ Sequence 2, Application US/10792517
/ Publication No. US20040152179A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Youle et al.
/ TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL
/ FILE REFERENCE: 4239-55417
/ CURRENT APPLICATION NUMBER: US/10/792,517
/ PRIOR FILING DATE: 2004-03-02
/ PRIOR APPLICATION NUMBER: US/09/639,245
/ PRIOR FILING DATE: 2000-08-15
/ PRIOR APPLICATION NUMBER: 60/149,220
/ PRIOR FILING DATE: 1999-08-16
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 411
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
```

```
/ OTHER INFORMATION: Description of Artificial Sequence: genetic fusion
US-10-792-517-2
```

```
Query Match
Best Local Similarity 39.9%; Pred. No. 2.4e-36;
Matches 93; Conservative 26; Mismatches 63; Indels 51; Gaps 4;
```

```
QY 11 RALVADPFGYKLRQKGY-----VCGAGP-----GEGRPA 39
DB 26 RELVDFLSYKLSQKGYSMQSPDSVDEENRTPEAGTESERETPSALINGNPSWHLADSPAV 85
QY 40 D-----PLHQAMRAAGDEFETFRRTSPDLAOLAHYPPGSAOQRTQ 81
DB 86 NGATMASSSLDAREVLPMAAVKQALREAGDEFEIKRYRAPSDLTSQHLITPGTAQYSPFEQ 145
QY 82 VSDLEFOGGEPMNGRLVAFVFGAALCAESVYKEMEPVGVQVODMVAYLETRRLADWIHSS 141
DB 146 VNVLEFRDGVNMGRIIVAFSFRGALCVESVDKEMQVLSRIASMMATYLDNDLEPWIQEN 205
QY 142 GGAFFETALYGGALAEERRLREGNMAVRYTLTGAVALGALVTVGAFFPASK 192
DB 206 GGMDTFVELYGNNAAESRKQGERFRNFWLTGMTVAGVLLGSLFSRKAYGAA 258
```

```
RESULT 14
US-10-402-017-4
/ Sequence 4, Application US/10402017
/ Publication No. US20030219871A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENBERGER
/ TITLE OF INVENTION: Host cells having improved survival properties and methods to gene
/ FILE REFERENCE: Case 1/1314
/ CURRENT APPLICATION NUMBER: US/10/402,017
/ PRIOR FILING DATE: 2003-03-28
/ PRIOR APPLICATION NUMBER: US 60/369,307
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 233
/ TYPE: PRT
/ ORGANISM: Cricetus griseus
US-10-402-017-4
```

```
Query Match
Best Local Similarity 42.6%; Score 429.5; DB 15; Length 233;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;
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```
QY 11 RALVADPFGYKLRQKGY-----V-----Y 28
DB 6 RELVDFLSYKLSQKGYSMQSPDSVDEENRTPEAGTESERETPSALINGNPSWHLADSPAV 65
```

```
QY 29 CGAGPGEGRPAD-----PLHOMRABAGDEFEFRPRTSDLAOLHVRPSGAQGRFT 80
Db 66 NGA-TGHSSSLDAREVYIPMAAVKQALRREGDEFEFLRYRPAASDLTSSQHLITPGTAYSFE 124
QY 81 QVDEFLFOGGPNNGRVLVAFFVFGAALCAESVKNKEMPIVGVOQDMVAVYLEETRLADVIHS 140
Db 125 QVAVNELFRDGVNNGRVLVAFFSFGALCVESVDKEMQVLASRASMATYLLNDHLEPIQD 184
QY 141 SGGMAEFTALYCGDALEEARLIRE--GNVASVRYLTJGATVALGAL 183
Db 185 NGCHDTFVELLYGNNAALAESRKGQERPNRNFLLGTMTVAGVILIGSL 229
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 10, 2005, 22:09:08 Search time 17 Seconds
(without alignments)
1092.343 Million cell updates/sec

Title: US-09-925-674B-9

Perfect score: 1009

Sequence: 1 MATPASPDPDRALVADPVG.....LTGAVLALGALVTGAFPAASK 193

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: PIR 79: *
2: PIR1: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------------|
| 1 | 428.5 | 42.5 | 233 | 2 | I49056 bcl-x long - mouse |
| 2 | 427.5 | 42.4 | 233 | 2 | B47537 apoptosis regulator |
| 3 | 424.5 | 42.1 | 233 | 2 | S51761 BCL-X protein - ra |
| 4 | 423.5 | 42.0 | 233 | 2 | A37332 transforming prote |
| 5 | 414 | 41.0 | 232 | 2 | S24390 transforming prote |
| 6 | 411.5 | 40.8 | 239 | 1 | TVHUB1 transforming prote |
| 7 | 411 | 40.7 | 236 | 2 | I67432 BCL-2 - rat (fragm |
| 8 | 406 | 40.2 | 236 | 2 | I53744 gene bcl-2 protein |
| 9 | 405 | 40.1 | 236 | 1 | TVMSA1 transforming prote |
| 10 | 404.5 | 40.1 | 233 | 2 | I67431 BCL-X-long - rat |
| 11 | 402 | 39.8 | 236 | 2 | JC7383 B-cell lymphoma 2 |
| 12 | 378 | 37.5 | 190 | 2 | A47537 apoptosis regulator |
| 13 | 377.5 | 37.4 | 214 | 2 | I49057 bcl-x transmembran |
| 14 | 374.5 | 37.1 | 227 | 2 | UB0203 apoptosis regula |
| 15 | 356 | 35.3 | 216 | 2 | B37332 transforming prote |
| 16 | 348.5 | 34.5 | 199 | 1 | TVMSB1 transforming prote |
| 17 | 345 | 34.2 | 205 | 1 | TVHUB1 transforming prote |
| 18 | 277.5 | 27.5 | 154 | 2 | I58194 gene bcl-2 protein |
| 19 | 182 | 18.0 | 170 | 2 | I49055 bcl-x short - mous |
| 20 | 174 | 17.2 | 176 | 2 | I67435 gene bcl-xshort pr |
| 21 | 171 | 16.9 | 211 | 2 | S58873 Bak protein - huma |
| 22 | 168 | 16.7 | 211 | 2 | S58875 ccdn-2 protein - hu |
| 23 | 158.5 | 15.7 | 192 | 2 | D47538 bcl-2-associated p |
| 24 | 154 | 15.3 | 192 | 2 | D47538 bcl-2-associated p |
| 25 | 151 | 15.0 | 261 | 2 | H88578 protein ced-9 (imp |
| 26 | 150.5 | 14.9 | 133 | 2 | A53189 apoptosis suppress |
| 27 | 147.5 | 14.6 | 179 | 2 | JC7255 Bax-delta protein |
| 28 | 147.5 | 14.6 | 218 | 2 | B47538 bcl-2-associated p |
| 29 | 147.5 | 14.6 | 218 | 2 | B47538 bcl-2-associated p |

| | | | | | |
|----|-------|------|------|---|-----------------------------|
| 30 | 142 | 14.1 | 177 | 2 | S54778 NR-13 protein - qu |
| 31 | 138.5 | 13.7 | 143 | 2 | I38921 bcl-2-associated p |
| 32 | 138 | 13.7 | 255 | 2 | JC7567 Mcl-1a protein - 2 |
| 33 | 136 | 11.5 | 175 | 2 | I39055 Bcl-2 related - hu |
| 34 | 116 | 11.5 | 350 | 2 | A47476 BCL2 homolog MCL1 |
| 35 | 105 | 10.4 | 122 | 2 | I49449 hemopoietic-specific |
| 36 | 88 | 8.7 | 185 | 2 | B83217 hypothetical prote |
| 37 | 87 | 8.6 | 343 | 1 | GNMWKV genome polyprotein |
| 38 | 86.5 | 8.6 | 301 | 2 | T36534 probable lipase/es |
| 39 | 86 | 8.5 | 270 | 2 | A12598 dihydrolipicolinat |
| 40 | 86 | 8.5 | 279 | 2 | B97381 glutamate-ammonia |
| 41 | 84.5 | 8.4 | 358 | 1 | AJLCOB alanyl-tRNA synthe |
| 42 | 83.5 | 8.3 | 872 | 2 | H95160 alanine-tRNA ligas |
| 43 | 83.5 | 8.3 | 872 | 2 | G98026 genome polyprotein |
| 44 | 83 | 8.2 | 3430 | 1 | GNMWKV beta-amyloid-like |
| 45 | 81.5 | 8.1 | 886 | 2 | A32758 |

ALIGNMENTS

RESULT 1
I49056
bcl-x long - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I49056; S52866
R/Fang, W.; Rivard, J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A/Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A/Reference number: I49055; MUID:95052604; PMID:7963517
A/Accession: I49056
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residue: 1-233 <RES>
A/Cross-references: UNIPROT:Q64373; EMBL:U0101; NID:9506647; PIDN:AAA82173.1; PID:G5066
R/Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
submitted to the EMBL Data Library, November 1994
A/Description: IL-5 inhibits anti-IGM-induced apoptosis in an immature B cell line throug
A/Reference number: S52866
A/Status: preliminary
A/Molecule type: mRNA
A/Accession: S52866
A/Status: preliminary
A/Residue: 1-233 <RAN>
A/Cross-references: EMBL:X83574; NID:9695622; PIDN:CAA58557.1; PID:9695623
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.5%; Score 428.5; DB 2; Length 233;
Best Local Similarity 41.3%; Pred. No. 1.8e-32;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADPVGKLRQKGY-----V 28
DB 6 RELVVDPLSKYKLSQKQSWGSPQSDVBNRTAEDETEARETPSAINGNSPMLADSPAV 65
QY 29 CGAGPGBGPAD-----ELHQAMRAAGDEBETPRRPSDLAQHLYTPGSAOORFT 80
DB 66 NGV-TGSSSLDAREVITPMAAVKQALREAGDEFLKRRRAFSPLTSLHTPGAVQSFE 124
QY 81 QVSEDELFOGQPMNQRVLVAFVFGAALCAESVNMEEPLVQVODMMWAVYLETLADWHS 140
DB 125 QVNEELPFGDSVMNGRIVAFSPFGALCVESVDDEMVLVSRISMAVYINDHLEPFIQE 164
QY 141 SGWMAEPTLYDGALBEARLRE--GNMAVETVLTGAVALLAL 183
DB 185 NGCMDTFVDLYGNMAAASRKRQGERFRNFWLTGMTVAGVLLGSL 229

RESULT 2
B47537
apoptosis regulator bcl-xl - human
N/Alternate names: bcl-2-related protein
N/Contains: apoptosis regulator bcl-xs

A/Molecule type: mRNA
 A/Residues: 1-232 <CA2>
 A/Cross-references: UNIPROT:Q00709; EMBL:Z11961; NID:962969; PIDN:CAA78018.1; PID:962970
 C/Superfamily: bcl apoptosis regulator, inhibitory type
 C/Keywords: mitochondrion; transmembrane protein

Query Match 41.0%; Score 414; DB 2; Length 232;
 Best Local Similarity 37.7%; Pred. No. 3.9e-31;
 Matches 86; Conservative 32; Mismatches 62; Indels 48; Gaps 4;

QY 9 DTRALVADPFGYKLRQKGYCGAG-----PGSGPAADP----- 41
 DB 10 DNREIVMKYIHYKLSQSGYEMWDGADGAPPAAPGIFSSQPGHTPHPAASDPVART 69
 QY 42 -----LHQAMRAAGDEFEFRFRFTFSDLAQLHTVTPGSAQORFTQVSD 85
 DB 70 LTVRCPLRGCAAPGPHALRQAGDEFRRYQDFAFMSQGLHTPTATGRFPAVVEE 129
 QY 86 LFQGGPMNGRLVAFVFGAALCAESVKNKEPVLGVQVDMVAVYLETRLADMDHSSGMA 145
 DB 130 LFRGVVWVRIVAFVFGGVWCVESVNRKMSPLVDNITMTETYLNRHLHMTIDNGMD 189
 QY 146 EFTALYDGDALBEARLRREGNMAVRYTLTGAVALGALTGVGAFPAK 193
 DB 190 AFVELYGN---SMRPLPFDPSWISLKTLS-LTVVGACITLTGAVLGHK 232

RESULT 6

TRANSFORMING protein bcl-2, splice form alpha - human

C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1988 #sequence revision 07-Jun-1996 #text change 09-Jul-2004
 C/Accession: C37332; A29409; S02452; A24428; A27622; B27622

R/Bguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues

A/Reference number: A37332; MUID:92375724; PMID:1508712

A/Accession: C37332

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-239 <EGU>

A/Cross-references: UNIPROT:P10415

A/Note: this report is a correction

R/Tsujimoto, Y.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

A/Title: Analysis of the structure, transcript, and protein products of bcl-2, the gene for the B-cell lymphoma

A/Reference number: A29409; MUID:86259760; PMID:3523487

A/Accession: A29409

A/Molecule type: mRNA

A/Residues: 1-95, 'A', 'G', '111-236', 'S', '238-239' <TSU>

A/Cross-references: GB:M13994; NID:9179366; PIDN:AAA51813.1; PID:9179367

A/Note: this sequence has been corrected in reference A37332

R/Seto, M.; Jaeger, U.; Hockett, R.D.; Grandinger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.

EMBO J. 7, 123-131, 1988

A/Title: Alternative promoters and exons, somatic mutation and deregulation of the bcl-2 gene

A/Reference number: S02452; MUID:80196071; PMID:2834197

A/Accession: S02452

A/Molecule type: mRNA

A/Residues: 1-239 <SET>

R/Cleary, M.L.; Smith, S.D.; Sklar, J.

Cell 47, 19-28, 1986

A/Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin heavy chain

A/Reference number: A24428; MUID:87002486; PMID:2875799

A/Accession: A24428

A/Molecule type: mRNA

A/Residues: 1-58, 'T', '60-116', 'R', '118-239' <CLB>

A/Cross-references: GB:M14745; NID:9179370; PIDN:AAA35591.1; PID:9179371

R/Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A.

Oncogene Res. 2, 263-275, 1988

A/Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma

A/Reference number: A27622; MUID:88217344; PMID:3285301

A/Accession: A27622

A/Molecule type: mRNA

A/Residues: 1-58, 'T', '60-239' <HUA>

A/Accession: B27622

A/Molecule type: DNA

A/Residues: 1-6, 'S', '8-58', 'T', '60-128', 'C', '130-239' <HUA2>

A/Note: the sequence was determined from the gemline gene

C/Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation

C/Genetics: GDB:BCL2

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Accession: B27622

A/Cross-references: GDB:119031; OMIM:151430

A/Map position: 18q21.3-18q21.3

C/Function: bcl apoptosis regulator, inhibitory type

A/Description: blocks apoptosis in hematopoietic cells

C/Superfamily: bcl apoptosis regulator, inhibitory type

C/Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 40.8%; Score 411.5; DB 1; Length 239;
 Best Local Similarity 37.0%; Pred. No. 7e-31;
 Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;

QY 9 DTRALVADPFGYKLRQKGYCGAG-----PGE----- 35
 DB 10 DNREIVMKYIHYKLSQSGYEMWDGADGAPPAAPGIFSSQPGHTPHPAASDPVART 69
 QY 36 -----GPAADP-----LHQAMRAAGDEFEFRFRFTFSDLAQLHTVTPGSAQOR 78
 DB 70 SPLQTPAAPGAAGPALSPPVPHVHLTRAGDQDFSRVYRDRFAEMSSQLHTPTARGR 129
 QY 79 FTVSDLEFQGGPMNGRLVAFVFGAALCAESVKNKEPVLGVQVDMVAVYLETRLADMD 138
 DB 130 FATVEELFRDGVWGRIVAFVFGGVWCVESVNRKMSPLVDNITMTETYLNRHLHMTIDNGMD 189
 QY 139 HSSGMAEFPAALYDGDALBEARLRREGNMAVRYTLTGAVALGALTGVGAFPAK 193
 DB 190 QDNGMDAFVELYGN---PSMRPLPFDPSWISLKTLSLAL-VGACITLTGAVLGHK 239

RESULT 7

BCL-2 - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text change 09-Jul-2004

C/Accession: 167432

R/Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.

Endocrinology 136, 232-241, 1995

A/Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equine

constitutive bcl-2 and bcl-x-long messenger ribonucleic acid levels.

A/Reference number: 153295; MUID:95129487; PMID:7828536

A/Accession: 167432

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-236 <RES>

A/Cross-references: UNIPROT:P49950; EMBL:U34964; NID:91004378; PIDN:AAA7687.1; PID:91004

C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.7%; Score 411; DB 2; Length 236;
 Best Local Similarity 36.2%; Pred. No. 7.6e-31;
 Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

QY 9 DTRALVADPFGYKLRQKGY----- 27
 DB 10 DNREIVMKYIHYKLSQSGYEMWDGDESDAPLRAPPGIFSPQESRTPAVHRDTART 69
 QY 28 -----VCGAGPESGPAADPLHQAMRAAGDEFEFRFRFTFSDLAQLHTVTPGSAQORFTQ 81
 DB 70 SPLRPLVANGPALSPPVPHVHLTRAGDQDFSRVYRDRFAEMSSQLHTPTARGRFAT 129
 QY 82 VSDLEFQGGPMNGRLVAFVFGAALCAESVKNKEPVLGVQVDMVAVYLETRLADMDHSS 141
 DB 130 VVELFRDGVWGRIVAFVFGGVWCVESVNRKMSPLVDNITMTETYLNRHLHMTIDNGMD 189
 QY 142 GMAEFPAALYDGDALBEARLRREGNMAVRYTLTGAVALGALTGVGAFPAK 193
 DB 190 GMDAFVELYGN---PSMRPLPFDPSWISLKTLSLAL-VGACITLTGAVLGHK 236

C:Genetics:
A:Gene: bcl-2
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: B-cell lymphoma; ovary

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 39.8% | Score 402; | DB 2; | Length 236; |
| Best Local Similarity | 35.3% | Pred. No. 5.3e-30; | | |
| Matches 82; | Conservative 34; | Mismatches 64; | Indels 52; | Gaps 3 |

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QY 9 DTATLVADEFGYTLARKGY----- 27
      | : : : | : |
Db 10 DNRKIWKYIHYTLSQLRGYEMVDGVDARLGAAPTRPGISFGQPSNTPRAVNHDMART 69
      | : : : | : |
QY 28 -----VCGAGPBGEPADPLDQAMRAGDEFETFRRTFSDLAQLHVTGSAQOBFQ 81
      | : : : | : |
Db 70 SPLRPIYALTGPTLSVPVPVHLLTLRRADDPSRRKRDPAEMSSQLHLTPFRARGPAT 129
      | : : : | : |
QY 82 VSDLEPQGGNNKRLVAFVFGALCAESVNMENEMERLVQGVQDDMMVALLEFRLDWTHSS 144
      | : : : | : |
Db 130 VVELLPFDGNNMRIRIAPFEPFGVNCVESVNMESPLVDNIALNMWTEYLNHHLTWIODN 189
      | : : : | : |
QY 142 GGAAPFTALVGDGLBEARLRREGNNAVSRYVTLTGVALGALVTVGAFFPAK 193
      | : : : | : |
Db 190 GGMDAPFELYG-----PSVAPRLPFPSHLSKTLISLAL-VGACITLTGYTLGK 236

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RESULT 12
A47537
apoptosis regulator bcl-x - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: A47537
R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Turkta, L.A.;
Cell 74, 597-608, 1993
A:Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptosis
A:Reference number: A47537; MUID:93364977; PMID:8358789
, A:Accession: A47537
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <BOI>
A:Cross-references: UNIPROT:007816; GB:I23110; GB:I20120; NID:g510898; PIDN:CAA80657.1;
C:Superfamily: bcl apoptosis regulator, inhibitory type

RESULT 13
149057
bcl-x transmembrane deleted - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49057
R:fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
U:Immunol. 153, 4388-4398, 1994
U:title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes

A:Reference number: I49055; MUID:95052604; PMID:7963517
A:Accession: I49057
A:Status: preliminary; translated from GB/EMBL/DBJ

| | | | | |
|-----------------------|------------------|------------------|------------|-------------|
| Query Match | 37.4%; | Score 377.5; | DB 2; | Length 214; |
| Best Local Similarity | 42.8%; | Pred. No. 9e-28; | | |
| Matches 80; | Conservative 16; | Mismatches 40; | Indels 51; | Gaps 3; |

QY 29 CGAGPREGPAAD-----PHTOMRAAGGEPFRPRRTSDLAALHTPGSAOGRFT 80
Db 66 NGA-TGHSSELDAREVITPMAAVKOLTRRGDEFEIETRRASDLSLTQHTPGTAYSFE 124
QY 81 QVSDDELFOGGPNWGRIVAFVFAGALCAESVNNKMEPLVGVQDWMVAYLETRLADPIHS 140
Db 125 QAVNELFRGVWNGRIVAFESFGALCAESVDKEMQVAVSIASMMATYINDHLEPIQR 184

| | | | |
|----|-----|---------|-----|
| QY | 141 | SGGWAEF | 147 |
| | : | | |
| Db | 185 | NGGWDTF | 191 |

```

RESULT 14
JB0203
apoptosis regulator bcl-x isoform - human
N|Alternate names: h-bcl-x-beta
C|Species: Homo sapiens (man)
C|Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C|Accession: JB0203
R|Ban, J.; Eckhart, L.; Wenzinger, W.; Mildner, M.; Techachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A|Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A|Reference number: JB0203; MUID:98340865; PMID:9675101
A|Accession: JB0203
A|Molecule type: mRNA
A|Residues: 1-227 <BAN>
A|Cross-references: UNIPROT:Q07817; GB:U73298; NID:g1622940; PIDN:AAB17354.1; PID:g16229
C|Genetics:
A|Gene: bcl-x
A|Map position: 20
C|Superfamily: bcl apoptosis regulator, inhibitory type

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Qy      11  RALVADPVGYKLRKRGY-----Y 28
Db      6  RELVADPFLSKYQKGYSMQPSDVEENRTAPEGTSSEMTPSAINGNPSMHLADSPAV 65

Qy      29  CGAGPEGEPAAD-----PLHQARRAGADEFTFRFRFTSDLAALAHYTPGSAOGRFT 80
Db      66  NGA-TGHSSLDARREVIPMAAVKQALRRAGDFEFLRRRAASDILTSQLHTTPGAAVSFE 124

Qy      81  QVSDDELFCQGGPNWGRIVAFPVFGAALCAESVYKMEKPELVGVQVDWVAAYLETRIADWTHS 140
Db      125  QVNNELFEFRGAVWGRIIVAFPSFGALCVESYDKEMQVLVRSIAAMATYINDHLEPIOE 184

Qy      141  SGGMAEFYALYGDGALIEBARR 161
Db      185  NGGMVRRTKPLVCPFSLASGQR 205

```

RESULT 15

B37332
 transforming protein (bcl-2-beta) - chicken
 C.Species: Gallus gallus (chicken)
 C.Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
 C.Accession: B37332; S35452
 R.Eguchi, Y.; Ewert, D.L.; Teujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A.Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues
 A.Reference number: A37332; MUID:92375724; PMID:1508712
 A.Accession: B37332
 A.Status: nucleic acid sequence not shown
 A.Molecule type: DNA
 A.Residues: 1-216 <ECU>
 A.Cross-references: EMBL:D11381; EMBL:D11382
 C.Superfamily: bcl apoptosis regulator, inhibitory type

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 35.3%; | Score 356; | DB 2; | Length 216; |
| Best Local Similarity | 38.4%; | Pred. No. 9.1e-26; | | |
| Matches 71; | Conservative 21; | Mismatches 49; | Indels 44; | Gaps 2; |

QY 9 DTBALVADFVGYTLRQGVYCGAG-----FGEGPADP----- 41
 Db 10 DNRREIYUKYTHYKLSRGIDMAAGEDRPVPAPAPAPAAPAVAANAAGASHHREPPGSA 69
 QY 42 -----LHQMRPAAGDEPETRFRFTSDLAQLHVTEGSAQOQFFQYSD 84
 Db 70 AASEVPPAEGELRAPPCVHIALRQACDEFSRKYQDFQMGSGQLHLTPFTYHGFVAWE 129
 QY 85 ELFGGEPNNGRVLAFFVFGAALCAESVYNKEMPTGVQYQDMMVAVYLETRLADWTIHSGGW 144
 Db 130 ELERFDVNNGRIVAAFEFGGVNVCVESVRENSPLVDNLTATMTETLYNRHLHNVIQDNGWM 189
 QY 145 AEFYA 149
 Db 190 VRACA 194

Search completed: April 10, 2005, 22:44:41
Job time : 17 secs